

OM protein - protein search, using bw model
Run on: February 23, 2005, 13:25:39 ; Search time 70,371 Seconds
(without alignmentB)
Title: US-10-622-817-2
Perfect Score: 1667
Sequence: I M K H Y Q V K P R Y H G G S A P R I V E L R H M R S C E N L A P R T N I K U K J 320
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Result No.	Score	Query Match Length	DB ID	Description
1	1667	100	0	ADBS8613 Human Pro
2	1667	100	0	ADMB0843 Tumour-as
3	1630	97	8	AAW25776 JTV1 prot
4	1630	97	8	ADR86551 1-312 ami
5	1378	82	7	ADCI10204 Human NOV
6	1191	74	229	ADR86553 84-312 am
7	832	49	9	ADR86552 1-161 ami
8	247	14	8	ABP01502 Human ORF
9	214.5	12	9	ABD62468 Drosophil
10	181	10	9	ABG23964 Novel hum
11	125.5	7	5	AAG41411 Arabidops
12	125.5	7	5	AAG41410 Arabidops
13	125.5	7	5	AAG41409 Arabidops
14	104	6	2	ABG62218 Drosophil
15	103	6	2	AAU04349 Mammalian
16	103	6	2	AAU79732 Human pro
17	103	6	2	AAU79716 Human pro
18	102	6	2	ADS24684 Bacterial
19	101	6	1	AAU10682 Polyhydro
20	101	6	1	AAU79440 Corynebac
21	101	6	1	AAU79989 Corynebac
22	101	6	1	AAU71908 C. glutam
23	101	6	1	AAU79739 Corynebac
24	101	6	1	AAU79988 Corynebac
25	101	6	1	AAU71907 C. glutam

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS	
RESULT 1	
ID	ABG80321
XX	ABG80321
AC	ABG80321
XX	C. glutamic acid
DT	2003-02-27
DE	Human Protein Q13155, SEQ ID NO 4489.
XX	
KW	Human; pain; neuronal tissue; gene therapy;
KW	spinal segmental nerve injury; chronic constriction injury; CCI;
KW	spared nerve injury; SNI; Chung.
OS	Homo sapiens.
XX	
PN	WO2003016475-A2.
XX	
PD	27-FEB-2003.
XX	
PF	14-AUG-2002; 2002WO-US025765.
XX	
PR	14-AUG-2001; 2001US-0312147P.
PR	01-NOV-2001; 2001US-0346382P.
PR	26-NOV-2001; 2001US-0333347P.
XX	
PA	(GEHO) GEN HOSPITAL CORP.
PA	(FARR) BAYER AG.
XX	
PI	Woolf C, Durso D, Beffort K, Costigan M;
XX	
DR	WPI; 2003-268312/26.
DR	GENBANK; Q13155.
XX	
PT	New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
PT	
PS	Claim 1; Page; 1017pp; English.
XX	
CC	The invention discloses a composition comprising two or more isolated rat or human poly nucleotides or a poly nucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel poly nucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the poly nucleotide sequence that is differentially expressed in neuronal tissue of a first animal
CC	

ID AAUW25776 standard; protein; 312 AA.
 XX
 AC
 XX AAUW25776;
 XX DT 19-DEC-1997 (first entry)
 XX DE JTV1 protein.
 XX KW JTV1; hPMs2; probe; detection; chromosome 7; deletion; mismatch repair gene; hereditary non-polyposis colorectal cancer; homologous recombination.
 XX OS Homo sapiens.
 XX PN WO9708312-A1.
 XX PD 06-MAR-1997.
 XX PP 26-AUG-1996; 96WO-US01398.
 XX PR 24-AUG-1995; 95US-00518862.
 XX PA (UYJO) UNIV JOHNS HOPKINS.
 XX PI vogelstein B, Kinzler KW, Nicolaides NC;
 XX DR N-PSDB; ATB6182.
 XX PT Novel chromosome 7 gene, JTV1 - used for detecting chromosome 7 deletions, and PMS2 promoter activity.
 XX PS Claim 5; Fig 2; 31pp; English.
 XX CC This sequence is JTV1 protein and is encoded by DNA isolated from human chromosome 7. The JTV1 coding sequence is located upstream from hPMs2. JTV1 cDNA can be used as probes to detect chromosome 7 deletions involving JTV1. Due to the overlapping promoter regions, deletions of JTV1 would also affect PMS2 (a mismatch repair gene) expression, leading to hereditary non-polyposis colorectal cancer. JTV1 can also be used to assay activity or competence of the PMS2 promoter region, the presence of JTV1 suggesting that the PMS2 promoter is intact. JTV1 sequences can also be used to guide homologous recombination at the PMS2 locus
 SQ Sequence 312 AA;

Query Match 97.8%; Score 1630; DB 2; Length 312;
 Best Local Similarity 100.0%; Pred. No. 4.3e-163; Mismatches 0; Indels 0; Gaps 0;
 Matches 312; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 MPMYQVPIYHGGGAPRLVELPTCMYRPNHGRSYGAPGAGHVOEESNLSQLAESRQD 60
 Db 1 MPMYQVPIYHGGGAPRLVELPTCMYRPNHGRSYGAPGAGHVOEESNLSQLAESRQD 60
 Qy 61 DIKRUYELKAAVDGLSKMOPPDAIDVTNTIQADEPTTUTNALDNLSVIGKDYGALK 120
 Db 61 DIKRUYELKAAVDGLSKMOPPDAIDVTNTIQADEPTTUTNALDNLSVIGKDYGALK 120
 SQ Sequence 312 AA;

Query Match 97.8%; Score 1630; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 4.3e-163; Mismatches 0; Indels 0; Gaps 0;
 Matches 312; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 YOLGFTLJWKNPKPTOMKFSOTMCPIEGEGNIAFLRSFLSGOKENAVNATLDSWDIA 240
 Db 1 YOLGFTLJWKNPKPTOMKFSOTMCPIEGEGNIAFLRSFLSGOKENAVNATLDSWDIA 240
 Qy 241 IFLKESSSKKEKAAPRSMNALSALKGSPLAGHETLADWVWNSVIQIGGSVTPANQ 300
 Db 241 IFLKESSSKKEKAAPRSMNALSALKGSPLAGHETLADWVWNSVIQIGGSVTPANQ 300
 Qy 301 RMRSCENLAPF 312
 Db 301 RMRSCENLAPF 312

RESULT 4
 ADR86551 ID ADR86551 standard; protein; 312 AA.
 XX AC ADR86551;
 XX DT 18-NOV-2004 (first entry)
 XX DE 1-312 amino acid sequence of p38/JTV-1 protein.
 XX KW p38/JTV-1; Cytostatic; cancer; leukemia; anticancer.
 XX OS Homo sapiens.
 XX PN EP1454628-A2.
 XX PD 08-SEP-2004.
 XX PR 09-SEP-2003; 2003EP-00020344.
 XX PR 03-MAR-2003; 2003KR-00013058.
 XX PA (UYSE-) UNIV SEOUL NAT IND FOUND.
 XX DR N-PSDB; AD886548.
 XX PT New isolated p38/JTV-1 protein, useful as medicament for treating cancer e.g., stomach, liver, blood, bone, pancreatic, skin, head or neck cancer and cutaneous or intraocular melanoma, as well as for screening new PT anticancer agents.
 XX PS Claim 5; SEQ ID NO 4; 47PP; English.
 CC The present invention relates to an isolated p38/JTV-1 protein for use as medicament. The p38/JTV-1 protein or the pharmaceutical composition is useful as medicament for treating breast cancer, large intestinal cancer, lung cancer, small cell lung cancer, stomach cancer, liver cancer, blood cancer, bone cancer, pancreatic cancer, skin cancer, head or neck cancer, cutaneous or intraocular melanoma, uterine sarcoma, ovarian cancer, rectal cancer, anal cancer, colon cancer, fallopian tube carcinoma, endometrial carcinoma, cervical cancer, vulval cancer, vaginal carcinoma, CC Hodgkin's disease, esophageal cancer, small intestine cancer, endocrine cancer, thyroid cancer, parathyroid cancer, adrenal cancer, soft tissue tumour, urethral cancer, penile cancer, prostate cancer, chronic or acute CC leukemia, lymphocytic lymphoma, bladder cancer, kidney cancer, uterine cancer, renal cell carcinoma, renal pelvic carcinoma, CNS tumour, primary CC CNS lymphoma, bone marrow tumour, brain stem nerve gliomas, pituitary adenoma, or their combination. The protein is useful as a target for screening new anticancer agents. The present sequence represents the 1-312 amino acid sequence of p38/JTV-1 protein.
 CC XX SQ Sequence 312 AA;

Query Match 97.8%; Score 1630; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 4.3e-163; Mismatches 0; Indels 0; Gaps 0;
 Matches 312; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 MPMYQVPIYHGGGAPRLVELPTCMYRPNHGRSYGAPGAGHVOEESNLSQLAESRQD 60
 Db 1 MPMYQVPIYHGGGAPRLVELPTCMYRPNHGRSYGAPGAGHVOEESNLSQLAESRQD 60
 Qy 61 DIKRUYELKAAVDGLSKMOPPDAIDVTNTIQADEPTTUTNALDNLSVIGKDYGALK 120
 Db 61 DIKRUYELKAAVDGLSKMOPPDAIDVTNTIQADEPTTUTNALDNLSVIGKDYGALK 120
 Qy 121 DIVINANPASPPPLSLVHLRJCEHFRVLSTVTHSSVKSVPENLLKCFGEONKKOPRD 180
 Db 121 DIVINANPASPPPLSLVHLRJCEHFRVLSTVTHSSVKSVPENLLKCFGEONKKOPRD 180
 Qy 181 YOLGFTLJWKNPKPTOMKFSOTMCPIEGEGNIAFLRSFLSGOKENAVNATLDSWDIA 240
 Db 1 YOLGFTLJWKNPKPTOMKFSOTMCPIEGEGNIAFLRSFLSGOKENAVNATLDSWDIA 240
 Qy 241 IFLKESSSKKEKAAPRSMNALSALKGSPLAGHETLADWVWNSVIQIGGSVTPANQ 300
 Db 241 IFLKESSSKKEKAAPRSMNALSALKGSPLAGHETLADWVWNSVIQIGGSVTPANQ 300
 Qy 301 RMRSCENLAPF 312
 Db 301 RMRSCENLAPF 312

QY 181 YOLGFTLWKNVKPTKOMFKS1OTMCPIEGENIARFLFLSLFGQKHNAWNTLIDSWDIA 240
 ||||| ||||| |||||
 ||||| VOLGFTLWKNVKPTKOMFKS1OTMCPIEGENIARFLFLSLFGQKHNAWNTLIDSWDIA 240
 PA (CURA-) CURAGEN CORP.
 PR XX
 PR PA
 PR PI Agee MI., Anderson DW, Berghes C, Casman SJ, Catterton E,
 PR PI Dibipio VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
 PR PI Gerlach VL, Gomian L, Guo X, Herrmann JL, Hilt T, Ji W, Kakuda R;
 PR PI Khramtsov NV, Li L, Liu X, Malvankar UM, Miller CB, Millet I;
 PR PI Ort T, Padigaru M, Paturajan M, Pena CEA, Rastelli L, Riiger DK;
 PR PI Rothenberg ME, Shenvy SG, Shimkets RA, Smithson G, Spaderna SK;
 PR PI Spyrek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
 PR PI Burgesse CE, Lepley DM;
 PR XX
 DR WPI; 2003-210149/20.
 DR N-PSDB; ADC10203.
 XX
 PT New isolated NOVX polypeptides and nucleic acid molecules useful for
 PT treating, preventing and diagnosing pathological conditions wth NOVX-
 PT associated disorders, such as cancer, obesity, diabetes and inflammatory
 PT or CNS diseases.
 PS Claim 1; SEQ ID NO 226; 772PP; English.
 XX
 CC The invention relates to novel isolated polypeptides, mature form of the
 CC polypeptide, a sequence that is 95% identical to the polypeptide or the
 CC polypeptide comprising one or more conservative substitutions. The NOVX
 CC polypeptide is useful for treating or preventing a pathology associated
 CC with the polypeptide e.g. disorders associated with aberrant expression
 CC or activity of the polypeptide, such as cancer, diabetes, obesity and
 CC endocrine, CNS and metabolic disorders. They can also be used in
 CC various detection and screening assays, chromosome mapping, tissue typing
 CC and predictive medicine. This sequence corresponds to one of the
 XX polypeptides of the invention.
 SQ Sequence 272 AA;
 PR Query Match 82.7%; Score 1378; DB 7; Length 272;
 PR Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 PR Matches 268; Conservative 0; Mismatches 0; Gaps 0;
 PR Indels 0; Gaps 0;
 PR 04-JUN-2001; 2001US-0295607P.
 PR 04-JUN-2001; 2001US-0295661P.
 PR 06-JUN-2001; 2001US-0296404P.
 PR 06-JUN-2001; 2001US-0296418P.
 PR 07-JUN-2001; 2001US-0296572P.
 PR 11-JUN-2001; 2001US-0297414P.
 PR 12-JUN-2001; 2001US-0295573P.
 PR 12-JUN-2001; 2001US-029567P.
 PR 14-JUN-2001; 2001US-0298283P.
 PR 15-JUN-2001; 2001US-0298528P.
 PR 18-JUN-2001; 2001US-0299133P.
 PR 19-JUN-2001; 2001US-0299230P.
 PR 21-JUN-2001; 2001US-0299949P.
 PR 22-JUN-2001; 2001US-0300177P.
 PR 26-JUN-2001; 2001US-0300883P.
 PR 28-JUN-2001; 2001US-0301530P.
 PR 03-JUL-2001; 2001US-0301550P.
 PR 31-JUL-2001; 2001US-0308830P.
 PR 14-SEP-2001; 2001US-0322297P.
 PR 25-SEP-2001; 2001US-032659P.
 PR 03-DEC-2001; 2001US-0337477P.
 PR 14-DEC-2001; 2001US-0341562P.
 PR 21-FEB-2002; 2002US-035856P.
 PR 21-FEB-2002; 2002US-0359122P.
 PR 22-FEB-2002; 2002US-0358978P.
 PR 22-FEB-2002; 2002US-0359034P.
 PR 22-FEB-2002; 2002US-0359035P.
 PR 22-FEB-2002; 2002US-0359121P.
 PR 27-FEB-2002; 2002US-0359864P.
 PR 01-MAR-2002; 2002US-0360858P.
 PR 12-MAR-2002; 2002US-0363430P.
 PR 12-MAR-2002; 2002US-0363676P.
 PR 10-APR-2002; 2002US-0371346P.
 PR 10-MAY-2002; 2002US-0379444P.

RESULT 5
 ADC10204
 ID ADC10204 standard; protein; 272 AA.
 AC ADC10204;
 DT 18-DEC-2003 (first entry)
 DE Human NOVX polypeptide SEQ ID NO: 226.
 DE cytostatic; antidiabetic; anorectice; cerebroprotective; neuroprotective;
 DE antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX;
 DE pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;
 DE inflammatory disorder; chromosome mapping; tissue typing;
 DE predictive medicine.
 OS Homo sapiens.
 XX WO2003000842-A2.
 XX PD 03-JAN-2003.
 XX SQ 04-JUN-2002; 2002WO-US017443.
 XX PR Query Match 82.7%; Score 1378; DB 7; Length 272;
 XX Best Local Similarity 100.0%; Pred. No. 1.6e-136;
 XX Matches 268; Conservative 0; Mismatches 0; Gaps 0;
 XX Indels 0; Gaps 0;
 PR 04-JUN-2001; 2001US-0295607P.
 PR 04-JUN-2001; 2001US-0295661P.
 PR 06-JUN-2001; 2001US-0296404P.
 PR 06-JUN-2001; 2001US-0296418P.
 PR 07-JUN-2001; 2001US-0296572P.
 PR 11-JUN-2001; 2001US-0297414P.
 PR 12-JUN-2001; 2001US-0295573P.
 PR 12-JUN-2001; 2001US-029567P.
 PR 14-JUN-2001; 2001US-0298283P.
 PR 15-JUN-2001; 2001US-0298528P.
 PR 18-JUN-2001; 2001US-0299133P.
 PR 19-JUN-2001; 2001US-0299230P.
 PR 21-JUN-2001; 2001US-0299949P.
 PR 22-JUN-2001; 2001US-0300177P.
 PR 26-JUN-2001; 2001US-0300883P.
 PR 28-JUN-2001; 2001US-0301530P.
 PR 03-JUL-2001; 2001US-0301550P.
 PR 31-JUL-2001; 2001US-0308830P.
 PR 14-SEP-2001; 2001US-0322297P.
 PR 25-SEP-2001; 2001US-032659P.
 PR 03-DEC-2001; 2001US-0337477P.
 PR 14-DEC-2001; 2001US-0341562P.
 PR 21-FEB-2002; 2002US-035856P.
 PR 21-FEB-2002; 2002US-0359122P.
 PR 22-FEB-2002; 2002US-0358978P.
 PR 22-FEB-2002; 2002US-0359034P.
 PR 22-FEB-2002; 2002US-0359035P.
 PR 22-FEB-2002; 2002US-0359121P.
 PR 27-FEB-2002; 2002US-0359864P.
 PR 01-MAR-2002; 2002US-0360858P.
 PR 12-MAR-2002; 2002US-0363430P.
 PR 12-MAR-2002; 2002US-0363676P.
 PR 10-APR-2002; 2002US-0371346P.
 PR 10-MAY-2002; 2002US-0379444P.

RESULT 6
 ADR8653
 ID ADR8653 standard; protein; 229 AA.
 AC ADR8653;
 DT 18-NOV-2004 (first entry)
 DE 84-312 amino acid sequence of p38/JTV-1 protein.
 KW p38/JTV-1; Cytostatic; cancer; leukemia; anticancer.
 XX

OS Homo sapiens.
 XX PN EP1454628-A2.
 XX PD 08-SEP-2004.
 XX PP 09-SEP-2003; 2003EP-00020344.
 XX PR 03-MAR-2003; 2003KR-00013058.
 XX PA (UYSE-) UNIV SEOUL NAT IND FOUND.
 XX PI Kim S, Park B;
 XX DR WPI; 2004-627822/61.
 XX N-PSDB; ADR86550.
 XX PT New isolated p38/JTV-1 protein, useful as medicament for treating cancer e.g., stomach, liver, blood, bone, pancreatic, skin, head or neck cancer and cutaneous or intraocular melanoma, as well as for screening new anticancer agents.
 XX PS Claim 5; SEQ ID NO 6; 47pp; English.
 CC The present invention relates to an isolated p38/JTV-1 protein for use as medicament. The p38/JTV-1 protein or the pharmaceutical composition is useful as medicament for treating breast cancer, large intestinal cancer, lung cancer, small cell lung cancer, stomach cancer, liver cancer, blood cancer, bone cancer, pancreatic cancer, skin cancer, head or neck cancer, cutaneous or intraocular melanoma, uterine sarcoma, ovarian cancer, rectal cancer, anal cancer, colon cancer, fallopian tube carcinoma, endometrial carcinoma, cervical cancer, vaginal carcinoma, Hodgkin's disease, esophageal cancer, small intestine cancer, endocrine cancer, bone cancer, pancreatic cancer, skin cancer, head or neck cancer, cutaneous or intraocular melanoma, uterine sarcoma, ovarian cancer, rectal cancer, anal cancer, colon cancer, fallopian tube carcinoma, endometrial carcinoma, cervical cancer, vaginal carcinoma, Hodgkin's disease, esophageal cancer, small intestine cancer, endocrine cancer, thyroid cancer, parathyroid cancer, adrenal cancer, soft tissue tumour, uterine cancer, penile cancer, prostate cancer, chronic or acute leukaemia, lymphocytic lymphoma, bladder cancer, kidney cancer, ureter cancer, renal cell carcinoma, renal pelvic carcinoma, CNS tumour, primary CNS lymphoma, bone marrow tumour, brain stem nerve gliomas, pituitary adenoma, or their combination. The protein is useful as a target for screening, new anticancer agents. The present sequence represents the 84-312 amino acid sequence of p38/JTV-1 protein.
 SQ Sequence 229 AA;

Query Match 71.4%; Score 1191; DB 8; Length 229;
 Best Local Similarity 100.0%; Pred. No. 7.2e-117;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 84 DADLDVNTIQADEPTLTNAIDLNSVLGKDYGALKDIVINANPASPPLSLVHLIC 143
 Db 1 DADLDVNTIQADEPTLTNAIDLNSVLGKDYGALKDIVINANPASPPLSLVHLIC 60

Qy 144 EPRFVISTVHTHSSVKSVPENILKCFGEQNKKQPRODQYQLGFTLWKNVPTQKMSIQT 203
 Db 61 EPRFVISTVHTHSSVKSVPENILKCFGEQNKKQPRODQYQLGFTLWKNVPTQKMSIQT 120

Qy 204 MCPIEGEGNIAFLFSLFGOKHNAVATLISWNDIAFOLKEKGSSKEKAFAFRSMNAL 263
 Db 121 MCPIEGEGNIAFLFSLFGOKHNAVATLISWNDIAFOLKEKGSSKEKAFAFRSMNAL 180

Qy 264 GKSPWMLAGNETWADVVLWVQIQQIGCSVTVPANYORMWMSCENTAPF 312
 Db 181 GKSPWMLAGNETWADVVLWVQIQQIGCSVTVPANYORMWMSCENTAPF 229

RESULT 7
 ADR86552
 ID ADR86552 standard; protein; 161 AA.
 XX
 AC ADR86552;
 XX
 DT 18-NOV-2004 (first entry)
 XX

DE 1-161 amino acid sequence of p38/JTV-1 protein.
 XX KW p38/JTV-1; Cytostatic; cancer; leukemia; anticancer.
 XX OS Homo sapiens.
 XX PN EP1454628-A2.
 XX PR 08-SEP-2004.
 XX PP 09-SEP-2003; 2003EP-00020344.
 XX PR 03-MAR-2003; 2003KR-00013058.
 XX PA (UYSE-) UNIV SEOUL NAT IND FOUND.
 XX PI Kim S, Park B;
 XX DR WPI; 2004-627822/61.
 XX N-PSDB; ADR86549.
 XX PT New isolated p38/JTV-1 protein, useful as medicament for treating cancer e.g., stomach, liver, blood, bone, pancreatic, skin, head or neck cancer and cutaneous or intraocular melanoma, as well as for screening new anticancer agent.
 RS Claim 5; SEQ ID NO 5; 47pp; English.
 CC The present invention relates to an isolated p38/JTV-1 protein or the pharmaceutical composition is useful as medicament for treating breast cancer, large intestinal cancer, lung cancer, small cell lung cancer, stomach cancer, liver cancer, blood cancer, bone cancer, pancreatic cancer, skin cancer, head or neck cancer, cutaneous or intraocular melanoma, uterine sarcoma, ovarian cancer, rectal cancer, anal cancer, colon cancer, fallopian tube carcinoma, endometrial carcinoma, cervical cancer, vaginal carcinoma, Hodgkin's disease, esophageal cancer, small intestine cancer, endocrine cancer, thyroid cancer, parathyroid cancer, adrenal cancer, soft tissue tumour, uterine cancer, penile cancer, prostate cancer, chronic or acute leukaemia, lymphocytic lymphoma, bladder cancer, kidney cancer, ureter cancer, renal cell carcinoma, renal pelvic carcinoma, CNS tumour, primary CNS lymphoma, bone marrow tumour, brain stem nerve gliomas, pituitary adenoma, or their combination. The protein is useful as a target for screening, new anticancer agents. The present sequence represents the 1-161 amino acid sequence of p38/JTV-1 protein.
 XX SQ Sequence 161 AA;

Query Match 49.9%; Score 832; DB 8; Length 161;
 Best Local Similarity 100.0%; Pred. No. 3.9e-79; Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPMYQVKPYHGGGAPRLVELPCTMYRILPNVIGRSYCPAPGAGHVQRENSLSIQALESRSQD 60
 Db 1 MPMYQVKPYHGGGAPRLVELPCTMYRILPNVIGRSYCPAPGAGHVQRENSLSIQALESRSQD 60

Qy 61 DIKRLYELKAVDGLSKMLOPDADLWNTIQADEPTLTNAIDLNSVLGKDYGALK 120
 Db 61 DIKRLYELKAVDGLSKMLOPDADLWNTIQADEPTLTNAIDLNSVLGKDYGALK 120

Qy 121 DIVINANPASPPLSLVHLICHEHFRVLSTVHTHSSVKS 161
 Db 121 DIVINANPASPPLSLVHLICHEHFRVLSTVHTHSSVKS 161

RESULT 8
 ABP01502
 ID ABP01502 standard; protein; 51 AA.
 XX
 AC ABP01502;
 XX
 DT 24-JUN-2002 (first entry)
 XX

DE Human ORFX protein sequence SEQ ID NO:2986.

KW XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; KW hyperproliferative disorder; psoriasis; benign tumour; hemorrhage; KW cardiovascular disease; osteoarthritis; neurodegenerative disorder; hypertension; hypothyroidism; diabetes mellitus; systemic lupus erythematosus; KW immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; myasthenia gravis.

KW OS Homo sapiens.

KW XX PN WO200192523-A2.

KW XX PD 06-DBCC-2001.

KW XX FF 29-MAY-2001; 2001WO-US010836.

KW XX PR 30-MAY-2000; 2000US-0206132P.

KW XX PR 29-AUG-2000; 2000US-0228716P.

KW PA (CURA-) CURAGEN CORP.

KW XX PI Shimkets RA, Leach MD;

KW XX PN WPI; 2002-106308/14.

KW DR N-PSDB; ABN17254.

KW XX PT Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.

KW XX PS Disclosure; SEQ ID NO 2986; 1037pp; English.

The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-1491 (see Table 1 in the specification). ABN1762 to ABN27252 encode the human ORFX protein given in ABP0010 to ABP1150. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder, and in the manufacture of a medicament for treating a syndrome associated with an ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, transplantation, cardiovascular diseases, disorders related to organ transplantation, cardiovacular disease, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, various diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, protection or regeneration and treatment of lung or liver fibrosis, systemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

KW XX SQ Sequence 51 AA;

KW XX Query Match 14.8%; Score 247; DB 5; Length 51;

KW Matches 49; Conservatve 1; Mismatches 1; Indels 0; Gaps 0;

KW XX Qy 74 DGLSKMIIQTPDADLIVNTIQADEPTTTLNDLNLSVKGKYGALKDIVI 124

KW Db 1 DGLSKMIIQTPDADLIVNTIQADEPTTTLNDLNLSVKGKYGALKDIVI 51

ID ABB62468 standard; protein; 334 AA.

ID XX AC ABB62468;

ID XX DT 26-MAR-2002 (first entry)

ID XX DE Drosophila melanogaster polypeptide SEQ ID NO 14196.

ID XX KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

ID XX OS Drosophila melanogaster.

ID XX PN WO200171042-A2.

ID XX PD 27-SEP-2001.

ID XX PR 23-MAR-2001; 2001WO-US009231.

ID XX PR 23-MAR-2000; 2000US-0191637P.

ID XX PR 11-JUL-2000; 2000US-00614150.

ID XX PA (PEKE) PE CORP NY.

ID XX PI Venter JC, Adams M, Li PW, Myers EW;

ID XX DR N-PSDB; ABL06571.

ID XX PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.

ID XX PS Disclosure; SEQ ID NO 14196; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABU6116-ABU30511), expressed DNA sequences (ABU0180-ABU1517), and the encoded proteins (ABB5773-ABB7072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

ID XX SQ Sequence 334 AA;

ID XX Query Match 12.9%; Score 214.5; DB 4; Length 334;

ID Matches 85; Conservatve 50; Mismatches 120; Indels 77; Gaps 10;

ID XX Qy 18 VELPFTCMRRLPNU---HGSYGPAGPAGHVSSESNISLQA-----

ID Db 13 IKUPFTCMPLAKNSLAADSASGSSTSASTASSTSSCKEADRDRGRNATCQLDLS 54

ID Qy 55 -----LESQDDILKLYELKLKAVDGHSKMTQTPDADLVDYNTIQADEPT 99

ID Db 73 LQRQIQLRLLKDDTAVAAKQEVQLKQLEBKLQQLGQR-----AGLGVG---KTFQT 99

ID Qy 100 TLTWNALDNLSVKGKYGALKDIVINANPAPSLSVLVRILLCEHRFLVSTVTHSSVK 159

ID Db 124 TAFQNG-----GLKEVPLQDVWVINGHPNPITPVALLKNAWRNLYTIDVKPFTSMA 176

ID Qy 160 SV-----PENIJKCGBONKKQPQDYQLGFTLWKQVPKYOMKFSIQTMPIEGEN 212

ID Db 177 DIGPAARSFEANIAKV---PVMPALK---LSVLIWNCHEHTEMISPTMVTPIGEVN 212

ID Qy 213 TARFLFSLFGQKHNAVATL---IDSWQDTAIFOLKECSKKAFAVFRSMISALGSPWL 230

ID Db 231 IIRYLGRGVPGABRYRGSPCLNEIDLVIDCYQIURCNCNTKTOVAMVRLUDRKRLQOYF 269

ID Qy 270 ASNELTADVWLSVUQQIGCSVWPNVQR 301

RESULT 9
ABB62468

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model
Run on: February 23, 2005, 13:36:20 ; Search time 17.81 Seconds

Perfect score: 1 MPMYQVKPYHGGGAPLRLVELPCTCMYKLPNVIGRSYCPAPGAHVQEESNLQALERSQQ 320
Sequence: BLOSUM62 Gapop 10.0 , Gapext: 0.5

Title: US-10-622-817-2
Perfect score: 1667
Sequence: 1 MPMYQVKPYHGGGAPLRLVELPCTCMYKLPNVIGRSYCPAPGAHVQEESNLQALERSQQ 320
Scoring table: BLOSUM62 Gapop 10.0 , Gapext: 0.5

Searched: 513545 seqb, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
Issued Patents AA:
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2: /cgnd2_6/prodata/1/1aa/*SB,_COMB_pep: *
3: /cgnd2_6/prodata/1/1aa/*6A,_COMB_pep: *
4: /cgnd2_6/prodata/1/1aa/*6B,_COMB_pep: *
5: /cgnd2_6/prodata/1/1aa/*PCRTUS,_COMB_pep: *
6: /cgnd2_6/prodata/1/1aa/*backfile1,pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Length	DB	ID	Description
1	1667	100.0	341	4	US-09-949-016-11312	Sequence 11312, A
2	1630	97.8	312	2	US-08-198-86C-2	Sequence 2, Appli
3	103	6.2	1512	3	US-09-443-184-48	Sequence 48, Appli
4	97	5.8	559	2	US-08-756-317-10	Sequence 10, Appli
5	97	5.8	559	4	US-09-091-609-4	Sequence 4, Appli
6	97	5.8	5215	3	US-09-105-537-2	Sequence 2, Appli
7	95	5.7	559	4	US-09-821-061-1	Sequence 1, Appli
8	95	5.7	559	4	US-10-259-632-1	Sequence 1, Appli
9	95	5.7	559	4	US-10-266-707-1	Sequence 1, Appli
10	92	5.5	2954	4	US-09-150-807-1	Sequence 1, Appli
11	91	5.5	474	4	US-09-248-796A-0321	Sequence 1, Appli
12	90.5	5.4	359	3	US-09-540-834-2	Sequence 2, Appli
13	90.5	5.4	597	1	US-08-399-636-102	Sequence 2, Appli
14	88.5	5.3	107	4	US-09-538-052-736	Sequence 102, App
15	88	5.3	427	4	US-09-949-016-11178	Sequence 736, App
16	88	5.3	724	4	US-09-900-930-62	Sequence 1178, A
17	88	5.3	883	4	US-09-328-523-9	Sequence 62, Appli
18	88	5.3	883	4	US-10-289-779B-2	Sequence 20321, A
19	88	5.3	914	4	US-09-976-239-9	Sequence 2, Appli
20	88	5.3	914	4	US-10-289-779B-4	Sequence 102, App
21	86.5	5.2	761	3	US-09-012-710-13	Sequence 1178, A
22	86.5	5.2	761	3	US-09-556-213-13	Sequence 62, Appli
23	86	5.2	211	4	US-09-328-523-9	Sequence 2, Appli
24	86	5.2	351	4	US-08-178-257-6	Sequence 6, Appli
25	86	5.2	471	3	US-09-134-001C-4904	Sequence 4904, Appli
26	86	5.2	1365	3	US-09-376-330-18	Sequence 18, Appli
27	86	5.2	5194600-4			

ALIGNMENTS

RESULT 1
US-09-949-016-11312
; Sequence 11312, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CI001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIORITY APPLICATION NUMBER: 60/241, 755
; PRIORITY FILING DATE: 2000-10-20
; PRIORITY APPLICATION NUMBER: 60/237, 768
; PRIORITY FILING DATE: 2000-10-03
; PRIORITY APPLICATION NUMBER: 60/231, 498
; PRIORITY FILING DATE: 2000-09-08
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11312
; LENGTH: 341
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11312

Query Match Similarity 100.0%; Score 1667; DB 4; Length 341;
Best Local Similarity 100.0%; Pred. No. 2.4e-181; Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY |||||MPMYQVKPYHGGGAPLRLVELPCTCMYKLPNVIGRSYCPAPGAHVQEESNLQALERSQQ 60
Dy |||||MPMYQVKPYHGGGAPLRLVELPCTCMYKLPNVIGRSYCPAPGAHVQEESNLQALERSQQ 81
22 MPMYQVKPYHGGGAPLRLVELPCTCMYKLPNVIGRSYCPAPGAHVQEESNLQALERSQQ 81
61 DILKRLYELKAUDGLSKMTOPTDADDVNTIQADEPTTUTTNALDLNSVIGKDYGALK 120
Dy |||||DILKRLYELKAUDGLSKMTOPTDADDVNTIQADEPTTUTTNALDLNSVIGKDYGALK 141
82 DILKRLYELKAUDGLSKMTOPTDADDVNTIQADEPTTUTTNALDLNSVIGKDYGALK 141
22 MPMYQVKPYHGGGAPLRLVELPCTCMYKLPNVIGRSYCPAPGAHVQEESNLQALERSQQ 81
61 DILKRLYELKAUDGLSKMTOPTDADDVNTIQADEPTTUTTNALDLNSVIGKDYGALK 120
Dy |||||DILKRLYELKAUDGLSKMTOPTDADDVNTIQADEPTTUTTNALDLNSVIGKDYGALK 141
121 DIVINANPASPLSLVLVHLCEHRFLSTWHTSSVSKWPENLILKCFGRONKKPRQD 180
Dy |||||DIVINANPASPLSLVLVHLCEHRFLSTWHTSSVSKWPENLILKCFGRONKKPRQD 201
142 DIVINANPASPLSLVLVHLCEHRFLSTWHTSSVSKWPENLILKCFGRONKKPRQD 201
QY 181 YOLGIFTIWKQVKPDKFSTQTMCPDEGEONIARFLPSLRFQKHINAVNATLDSWIDIA 240
Dy |||||YOLGIFTIWKQVKPDKFSTQTMCPDEGEONIARFLPSLRFQKHINAVNATLDSWIDIA 261
202 YOLGIFTIWKQVKPDKFSTQTMCPDEGEONIARFLPSLRFQKHINAVNATLDSWIDIA 261
Dy |||||YOLGIFTIWKQVKPDKFSTQTMCPDEGEONIARFLPSLRFQKHINAVNATLDSWIDIA 261
241 IFOLKEGSSKEKAAYFVRSMSALGKSPWLQAGNELTAVDVVLWSVLOQIGGCSVTVPANVQ 300
Dy |||||IFOLKEGSSKEKAAYFVRSMSALGKSPWLQAGNELTAVDVVLWSVLOQIGGCSVTVPANVQ 300
262 IFOLKEGSSKEKAAYFVRSMSALGKSPWLQAGNELTAVDVVLWSVLOQIGGCSVTVPANVQ 321
Dy |||||IFOLKEGSSKEKAAYFVRSMSALGKSPWLQAGNELTAVDVVLWSVLOQIGGCSVTVPANVQ 321

301 RWMRSCENLAPFTALKLK 320

Db 322 RWMRSCENLAPPNTALKLK 341

RESULT 2

US-08-518-862C-2

Sequence 2, Application US/0851862C

Patent No. 5843757

GENERAL INFORMATION:

APPLICANT: Vogelstein, Bert

APPLICANT: Kinzler, Kenneth W.

APPLICANT: Nicolaides, Nicholas C.

TITLE OF INVENTION: Human JIV1 Gene Overlaps PMS2 Gene

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Witcoff, Ltd.

STREET: 1001 G Street, N.W.

CITY: Washington, D.C.

COUNTRY: U.S.A.

ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/518,862C

FILING DATE: 24-AUG-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 01107.49697

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9299

TELEFAX: 202-508-9299

INFORMATION FOR SEQ ID NO: 2:

SEQUENCER CHARACTERISTICS:

LENGTH: 312 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-518-862C-2

Query Match 97.8%; Score 1630; DB 2; Length 312;

Best Local Similarity 100.0%; Pred. No. 3.5e-177; Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPMYQVKIHYGGAPRLRVELLPTCMYLRPNVIGRSYGRPAAGHGVORESNUQSLESDQ

Db 1 MPMYQVKIHYGGAPRLRVELLPTCMYLRPNVIGRSYGRPAAGHGVORESNUQSLESDQ

Qy 61 DIKRLYELKAADVGLSKMIDPDAEDVTTIQADEPTTITNADLNSVLGQDYGALK 60

Db 61 DIKRLYELKAADVGLSKMIDPDAEDVTTIQADEPTTITNADLNSVLGQDYGALK 60

Qy 121 DIVINANPASPLAVTHRLICEHERPVLSVTHHSVSVPENLKQPGEQNKQPRQD 120

Db 121 DIVINANPASPLAVTHRLICEHERPVLSVTHHSVSVPENLKQPGEQNKQPRQD 120

Qy 181 YOLGFTLWIKVPKYKTMKFSTQTMPIERGNGIARPLFSLFGQKHNAVATLDSWDIA 240

Db 181 YOLGFTLWIKVPKYKTMKFSTQTMPIERGNGIARPLFSLFGQKHNAVATLDSWDIA 240

Qy 241 FOLKEGSSKREKAAYERSMSALGKSPMLAGNETVADVLMSVLLQQTGCCTVPANQ 300

Db 241 FOLKEGSSKREKAAYERSMSALGKSPMLAGNETVADVLMSVLLQQTGCCTVPANQ 300

Qy 301 RWMRSCENLAPP 312

Db 301 RWMRSCENLAPP 312

RESULT 3

US-08-443-184-4B

Sequence 48, Application US/09443184A

Patent No. 6372431

GENERAL INFORMATION:

APPLICANT: Cunningham, Mary Jane

APPLICANT: Zweiger, Gary

APPLICANT: Kaser, Matthew R.

APPLICANT: Panzer, Scott

APPLICANT: Seilhamer, Jeffrey J.

APPLICANT: Yue, Henry

APPLICANT: Azimzai, Yalda

APPLICANT: Ial, Preeti

TITLE OF INVENTION: MAMMALIAN TOXICOLOGICAL RESPONSE MARKERS

CURRENT FILING DATE: 1999-11-19

FILE REFERENCE: PCC-0007 US

CURRENT APPLICATION NUMBER: US/09/443,184A

SEQ ID NO: 138

SEQ ID NO: 48

LENGTH: 1512

TYPE: PRT

FEATURE:

ORGANISM: Homo sapiens

NAME/KEY: misc. feature

OTHER INFORMATION: Incyte ID No. 6372431 2302721CD1

US-09-443-184-4B

Query Match 6.2%; Score 103; DB 3; Length 1512;

Best Local Similarity 22.1%; Pred. No. 0.12; Matches 45; Conservative 30; Mismatches 69; Indels 60; Gaps 9;

Db 124 INANPASPPLSLVLRHLICERFRVISTVHHSVSYKSVPENLKQPGEQNKQPRQDQL 183

Db 6 LTNSGDPIGAL---LAVERHKDVS1---SVEGKENILH----41

Qy 184 GFTLUWKVPKYKTMKFSTQTMPIERGNGIARPLFSLFGQKHNAVATLDSWV 237

Db 42 ---VSENVIFDV-----NSIRYLARVATAGLVGS--NLMEPEIDWL 82

Qy 238 DIAFOKEKGSKESKEAKFVFSMSALGKSPMLAGNETADVWVSVLQOIGCWS---- 292

Db 83 EFSATKL---SSCDSFNSTINBINHCLSLRTRYLVNSLSDLCWATIK--GMAWOBQ 138

Qy 293 --VTVPANQWRMRSCENLAPP 314

Db 139 KQKCAPVHKEWFGLFLEAQAFQ 162

RESULT 4

US-08-756-317-10

Sequence 10, Application US/08756317

Patent No. 5494984

GENERAL INFORMATION:

APPLICANT: Clemente, Thomas E.

APPLICANT: Kishore, Ganesh M.

APPLICANT: Mitsky, Timothy A.

APPLICANT: Stark, David M.

TITLE OF INVENTION: Improved Rhodospirillum Rubrum

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2005, 13:57:26 ; Search time 50.2443 Seconds

Sequence: 1 MPMYQVVKYHGGGAPRLVEL... RWRSCENLAPNTALKLK 320 (without alignments)

Scoring table: BLOSUM62 2084.158 Million cell updates/sec

Title: US-10-622-817-2

Perfect score: 1667

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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 2: /cggn2_6/podata/1/pubpaas/PCTC_NEW_PUB.pep: *
 3: /cggn2_6/podata/1/pubpaas/US06_NEW_PUB.pep: *
 4: /cggn2_6/podata/1/pubpaas/US05_PUBCOMB.pep: *
 5: /cggn2_6/podata/1/pubpaas/US07_NEW_PUB.pep: *
 6: /cggn2_6/podata/1/pubpaas/PCUTS_PUBCOMB.pep: *
 7: /cggn2_6/podata/1/pubpaas/US08_NEW_PUB.pep: *
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 9: /cggn2_6/podata/1/pubpaas/US09_PUBCOMB.pep: *
 10: /cggn2_6/podata/1/pubpaas/US10C_PUBCOMB.pep: *
 11: /cggn2_6/podata/1/pubpaas/US09C_PUBCOMB.pep: *
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 14: /cggn2_6/podata/1/pubpaas/US10B_PUBCOMB.pep: *
 15: /cggn2_6/podata/1/pubpaas/US10C_PUBCOMB.pep: *
 16: /cggn2_6/podata/1/pubpaas/US10D_PUBCOMB.pep: *
 17: /cggn2_6/podata/1/pubpaas/US10I_NEW_PUB.pep: *
 18: /cggn2_6/podata/1/pubpaas/US11_NEW_PUB.pep: *
 19: /cggn2_6/podata/1/pubpaas/US60_NEW_PUB.pep: *
 20: /cggn2_6/podata/1/pubpaas/US60_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1630	97.8	312	16 US-10-463-676-4 Sequence 4, Appli
2	1191	71.4	229	16 US-10-463-676-6 Sequence 6, Appli
3	832	49.9	16	16 US-10-463-676-5 Sequence 5, Appli
4	102	6.1	201	15 US-10-369-493-13717 Sequence 13717, A
5	6	6.1	826	10 US-09-746-660A-92 Sequence 92, Appli
6	6	6.1	833	10 US-09-746-660A-92 Sequence 90, Appli
7	6	6.1	1221	9 US-09-919-891-2 Sequence 2, Appli
8	101	6.1	1221	9 US-09-738-661-5163 Sequence 5163, AP
9	101	6.1	1221	15 US-10-450-055-2 Sequence 2, Appli
10	101	6.1	1221	17 US-10-494-675-156 Sequence 156, AP
11	100.5	6.0	687	15 US-10-425-1458897 Sequence 58897, A
12	100.5	6.0	1200	15 US-10-282-122A-53993 Sequence 53993, A
13	97.5	5.8	652	15 US-10-264-049-3001 Sequence 3001, AP

ALIGNMENTS

```

RESULT 1
US-10-463-676-4
; Sequence 4, Application US/10463676
; Publication No. US20040175375A1
; GENERAL INFORMATION:
  APPLICANT: Kim, Sungsoon
  APPLICANT: Park, Bum-Joon
; TITLE OF INVENTION: Method for Treating Cancer Using P38/JTV-1 and Method
; TITLE OF INVENTION: for Screening Pharmaceutical Composition for Treating Cancer
; FILE REFERENCE: 012670-09A
; CURRENT APPLICATION NUMBER: US/10/463, 676
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: KR 10-2003-113058
; NUMBER OF SHO ID NOS: 17
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEO ID NO 4
LENGTH: 312
; TYPE: BRT
; ORGANISM: Homo sapiens
FEATURE:
; NAME/KEY: PEPTIDE
LOCATION: (312)
; OTHER INFORMATION: 1-312 amino acid sequence of p38/JTV-1
US-10-463-676-4
Query Match Score: 97.8%; Pred. No. 6.4e-153; Length: 312;
Best Local Similarity 100.0%; Minmatches: 0; Indels: 0; Gaps: 0;
Matches: 312; Conservative: 0;

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QY 1 MPMYQVVKYHGGGAPRLVELPTCMRILPVGIGRSICGPGAGHVGQESNLQALESRQD 60

QY 1 MPMYQVVKYHGGGAPRLVELPTCMRILPVGIGRSICGPGAGHVGQESNLQALESRQD 60

Db 1 MPMYQVVKYHGGGAPRLVELPTCMRILPVGIGRSICGPGAGHVGQESNLQALESRQD 60

QY 61 DILKRLYELKAADVGLSKMIDPADDIVTIIQADPPTLTNTAALDLNSVLGKDYGALK 120

A;Gene: ANSP:F21E10.12
A;Map position: 5
A;Introns: 47/2; 89/3; 141/1; 503/3; 659/3
C;Superfamily: Yeast glutamate-tRNA ligase; glutamine-tRNA synthetase; ligase; protein biosynthesis
C;Keywords: aminoacyl-tRNA synthetase; ligase; homology <EGL>
F;223-499;Domain: glutamine-tRNA ligase homology

Query Match 6.7%; Score 111; DB 2; Length 728;
Best Local Similarity 25.9%; Pred. No. 0.3%; Mismatches 53; Indels 58; Gaps 10;
Matches 48; Conservative 26; C:Keywords: transferase

Qy 128 PASPPLSVLVAHLICHEFRVLTWTHS3VSKVSPENLLKFGGEONKKPQQDQVOLGFL 187
Db 10 PESPPPLSVLVAHLICHEFRVLTWTHS3VSKVSPENLLKFGGEONKKPQQDQVOLGFL 187
Qy 188 IWKNNPEKTMKFPSIQTMCPEGEQHIAREFLSLGOKHNNAVT-----LIDSWD 238
Db 56 LILRYV-----GKSAKPKDPYQ---NNAFDSSQSVLICINMKIDENWD 95
Qy 239 IA-IFOLKEGSSEKKAFFMSNSALGKSPWLAGNELTADVVWSVLOQIGGCVTVPA 297
Db 96 YASVF--SSGSEFENAC--GRVDKYLESTFLVHSLSTDVAIWSLAGTG----- 143
Qy 298 NVQRW 302
Db 144 --QRW 146

RESULT 3

G82441
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: G82441
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Richardson, D.; Raskin, R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
L;R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: G82441
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-222 <HEI>
A;Cross-references: UNIPROT:09K005; GB:AB004389; GB:AE003853; NID:99657989; PIDN:AAF9648
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCA0584
A;Map position: 2
C;Superfamily: hypothetical protein b2302

Query Match 6.3%; Score 105.5; DB 2; Length 222;
Best Local Similarity 25.7%; Pred. No. 0.17%; Mismatches 28; Conservative 22; Indels 21; Gaps 4;
Matches 28; C:Keywords: transferase

Qy 197 MKPSIQTMCPPIEGEGNARFLSLFGOKHNNAVTIDLSDWMDIAFOLKEGSSEKKAFF 256
Db 97 LMFOOMSGVGPMQANV---FTRYPEKIQPA---IDRY-----QKGRRLF 137
Qy 257 RSMSNLGKSPPMAGNELTADVVL--WSVUQIGGCSVTANVORMW 303
Db 138 FVMDGQLAQNPVLAGDVTIADIATFPWVRHEWSGISIDGSLTHLQRWM 186

RESULT 4

A29035
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A29036
R;Abamovitz, M.; Listowsky, I.
J; Biol. Chem. 262, 7770-7773, 1987
A;Title: Selective expression of a unique glutathione S-transferase Yb3 gene in rat brain

A;Reference number: A29036; MUID:87222405; PMID:3584141
A;Accession: A29036
A;Molecule type: mRNA
A;Cross-references: UNIPROT:P09009; GB:J02744; NID:9204512; PID:920451
C;Superfamily: glutathione transferase
C;Keywords: transferase

Query Match 5.8%; Score 97.5; DB 2; Length 218;
Best Local Similarity 25.6%; Pred. No. 0.78%; Mismatches 33; Conservative 24; Indels 41; Gaps 5;
Matches 33; C:Keywords: transferase

Qy 179 QDYQOLGFTLTIWKNKVKPQMKFSIQTMCPIEGEGNATARFLSLFGOKHNNAVT----- 231
Db 49 EFKKLG--LDFPNLP-----YLIDGSHKTTOSNATIRYL---GRKHNLCGETBEER IRV 97
Qy 232 -----LIDSWDIA-----IFQKEGSSEKKAFFMSNSALGKSPWLAGNELTADV 278
Db 98 DILENQIMDNRNWMLARLYCNPDFFEKULPGYLEQPGMMRLYSEPLGKRPWFAGDKITFVD 157
Qy 279 VULMSVHQ 287
Db 158 FTAYDVLER 166

RESULT 5

JC5517
Gu/RNA helicase II binding protein - human
C;Species: Homo sapiens (man)
C;Accession: JC5517
R;Valdez, B.C.; Henning, D.; Perkaly, L.; Busch, R.K.; Busch, H.
Biochem. Biophys. Commun. 234, 315-340, 1997
A;Title: Cloning and characterization of Gu/RH-II binding protein.
A;Reference number: JC5517; MUID:97320420; PMID:917771
A;Accession: JC5517
A;Molecule type: mRNA
A;Residues: 1-645 <VAL>
A;Cross-references: GB:U78524; NID:91696006; PIDN:AB58488.1; PID:91696007
A;Note: it is uncertain whether Met-4 or Met-6 is the initiator
C;Comment: This protein is localized to the nucleus and interacts with Gu/RNA helicase I
C;Keywords: phosphoprotein
F;50-58/Region: nuclear location signal
F;362-374/Region: nuclear location signal
F;514-515,51-554,592-595,606-609/Region: 4-residue repeats (N-T-S-L)
F;7,177,322,412,432,460,461,462,470,614,627/Binding site: phosphate (Ser) (covalent) #status predicted
F;65,394,624/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 5.8%; Score 97.5; DB 2; Length 645;
Best Local Similarity 20.5%; Pred. No. 3.7%; Mismatches 79; Conservative 56; Indels 121; Gaps 20;
Matches 79; C:Keywords: transferase

Qy 16 LRV-ELPTCM-YRIPNVHGRGSRVGPAGGHVQBESENLSQALESRQDDILKLYELKA 73
Db 8 LRVSBLQVQVLYAGRNGKRGKRGHLKLLKAG---CSPAYOMKTKELYRFRFQK--- 62
Qy 74 DGLSKMIDTPDAIDLVTIIOADEPTTITNALDLSVLGKDGYALKDIVNAPASPP 133
Db 63 -----IMPP-ADLSIPVNWHSSBMPATPS-----TIPQLTVDGHPASSPL 102
Qy 134 ---SLI-WARLICHEFRVLSVTHS3VSKVSP-----ENIJK-CFGEBONKKQ---- 176
Db 103 LPVSLIGHKGELPHLPHLTSALHPVHDPLKQPLPFUDLDELIKPTSLASNDRPRETC 162
Qy 177 -----PRDQYOLGFTLTIWKNKVKPQMKFSIQTMCPIEGEG----- 211
Db 163 FAFLTPOQVQOISSSM---DISGTRCDFTVQVRLCSETSCPDHFPNLCVRNT 219
Qy 212 -----NARFLSLFGOKHNNAVTIDLSDW-----DI 239
Db 220 KPCSLPGYLPPTRKNGVERKRSRSPNITSLV---RLSTTPNTIVWSMAEIGRNYSM 274
Qy 240 AFQKRESS-----KEKAFFMSNSALGKSPWLAGNELTADVVL-WSVUQIGGC 291

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.									
OM protein - protein search, using sw model									
Run on: February 23, 2005, 13:33:04 ; Search time: 60.8145 seconds									
(without alignment) 2694.512 Million cell updates/sec									
Title: US-10-622-817-2	Perfect score: 1667	Sequence: 1 MPMYQVKPHGGGAPRLVEL. RMMRSCENLAPNTALKLK 320	Scoring table: BLOSUM62	Gapop: 10.0 , Gapext: 0.5	Searched: 1612378 seqs, 512079187 residues				
Total number of hits satisfying chosen parameters: 1612378									
Minimum DB seq length: 0									
Maximum DB seq length: 200000000									
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries									
Database :	UniProt 03:*								
1: uniprot_sprot:*	2: uniprot_trembl:*								
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	Query Match Length	DB ID	Description	RT	RN	RP	RX	RA
1	1667	100.0	320	MCA2_HUMAN	MC2_HUMAN	STANDARD;	PRT;	320 AA.	
2	1663	99.8	320	Q96Z5 Homo sapien	ID=MCA2_HUMAN				
3	1464	87.8	320	Q8R010 mus musculus	AC=Q3155; QSP112;				
4	1464	87.8	320	Q8P2Y6 mus musculus	DT=01-NOV-1997 (Rel. 35, Created)				
5	1444	86.6	320	1 MCA2_CRIGR	DT=16-OCT-2001 (Rel. 40, Last sequence update)				
6	1260	75.6	280	Q8R3V2 mus musculus	DT=05-JUL-2004 (Rel. 44, Last annotation update)				
7	1144.5	68.7	311	2 Q6DX86 xenopus tro	DE=Multisynthetase complex auxiliary component p38 (JTV-1 protein)				
8	139.5	68.4	311	2 Q6IN04 xenopus lae	DB=(PRO0992)				
9	1312.5	67.9	311	2 Q7ZYD7 xenopus lae	Name=JTV1;				
10	887.5	53.2	321	2 Q7T3C0 brachydanio	OS=Homo sapiens (Human).				
11	267.5	16.0	340	2 Q7QTA3 anophelles g	OC=Bacteria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
12	224	13.4	301	2 Q7KUM5 drosophila	OC=Mammalia; Butheria; Primates; Catarrhini; Homidae; Homo.				
13	224	13.4	313	2 Q8TO60 drosophila	OX=NCH-1; TAXID=9606;				
14	224	13.4	322	2 Q6NQ04 drosophila	RN=[1]				
15	214.5	12.9	334	1 MCA2_DROME	SEQUENCE FROM N.A.				
16	225.5	7.5	719	2 Q8A462 drosophila	RP=MEDLINE:96115582; PubMed=8666379;				
17	111	6.7	728	2 Q6S253 arabiadopsis	RT=				
18	106.5	6.4	880	2 Q8EPT1 oceanobacil	RA="Analysis of the 5' region of the pMS2 reveals heterogeneous transcripts and a novel overlapping gene.;"				
19	106.5	6.4	913	2 Q6DRB3 oceanobacil	RT=				
20	106.5	6.4	913	2 Q6PFQ4 brachydanio	RL=Genomics 29:329-334(1995).				
21	105.5	6.3	913	2 Q9KNO5 vibrio chol	RN=[2]				
22	105	6.3	240	2 Q8BT1I drosophila	SEQUENCE FROM N.A.				
23	105	6.3	1512	1 SYEP_MOUSE	RP=RC				
24	105	6.3	1800	2 Q7PRF2 anophelles g	RT=TISSUE=Fetal liver;				
25	104.5	6.3	922	2 Q6TM85 brachydanio	RT="Generation and initial analysis of more than 15,000 full-length human				
26	104	6.2	661	2 Q9VB85 drosophila	RT=RT				
27	104	6.2	702	2 Q8THC6 drosophila	RN=RA				
28	104	6.2	841	2 Q8TMQ2 drosophila	RA=Liu M., He F.,				
29	103	6.2	328	2 Q86X73 homo sapien	RA="Functional prediction of the coding sequences of 121 new genes deduced by analysis of cDNA clones from human fetal liver.";				
30	103	6.2	865d79	homo sapien	RT=Submitted (DBC-1998) to the EMBL/GenBank/DBJ databases.				
31	103	6.2	1213	2 Q8FTD2 cornebacte	RN=[4]				

RESULT 3			
OBR010	OBR010; PRELIMINARY;	PRT;	320 AA.
ID	Q8R2Y6	PRELIMINARY;	320 AA.
AC	Q8R2Y6;		
OBR010;	OBR010; PRELIMINARY;		
DT	01-JUN-2002 (TREMBREL. 21, Created)		
DT	01-JUN-2002 (TREMBREL. 21, Last sequence update)		
DT	05-JUL-2004 (TREMBREL. 27, Last annotation update)		
DE	Jtv1-pending protein.		
GN	Name=Jtv1;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxId=10090;		
RN	[1] PREQUENCE FROM N_A.		
RP	SEQUENCE FROM N_A.		
RC	STRAIN=FVB/N, and FVB/N-3; TISSUE=Mammary tumor;		
RX	MEDLINE=22388257; PubMed=1477932; DOI=10.1073/pnas.242503899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altshul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Tsohbyki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RN	[2] PREQUENCE FROM N_A.		
RP	SEQUENCE FROM N_A.		
RC	STRAIN=FVB/N; TISSUE=Mammary tumor; C3;		
RA	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.		
RL	RN [3]		
RN	SEQUENCE FROM N_A.		
RC	STRAIN=FVB/N-3; TISSUE=Mammary tumor;		
RA	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.		
RL	RN [4]		
DR	MCD; MGI:2385237; Jtv1; InterPro; IPR00446; GST_C-term.		
DR	InterPro; IPR010987; GST_C-like.		
DR	pFam; PF00043; GST_C; 1;		
SQ	SEQUENCE 320 AA; 35396 MW; 1745DTEB4BC3670D CRC64;		
Qy	Query Match Best Local Similarity 87.8%; Score 1464; DB 2; Length 320; Matches 279; Conservative 16; Mismatches 25; Indels 0; Gaps 0;		
Db	1 MPMYQVKYHGGGAPRLVPLPTCMRVLVHLLCERFLVSTVTHSSKTSKVPEPNLICFGEOQNKKQPROD 60		
Qy	61 DILKRLYELKAADVGLSKMIQTPDAADLVNTIQADEPTLTNALDIANSVIGKDYGALK 120		
Db	61 DILKRLYELKAADVGLSKMIQTPDAADLVNTIQADEPTLTNALDIANSVIGKDYGALK 120		
Qy	181 YOLGFTLWKVNKTQMKPSITQMPICSEGNTARFLSLFGOKHNAVNLDSWUDIA 240		
RESULT 4			
ID	Q8R2Y6	PRELIMINARY;	320 AA.
AC	Q8R2Y6;		
DT	01-JUN-2002 (TREMBREL. 21, Created)		
DT	01-JUN-2002 (TREMBREL. 21, Last sequence update)		
DT	01-MAR-2004 (TREMBREL. 26, Last annotation update)		
DE	Jtv1-pending protein.		
GN	Name=Jtv1;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxId=10090;		
RN	[1] PREQUENCE FROM N_A.		
RP	SEQUENCE FROM N_A.		
RC	STRAIN=CZECH II, TISSUE=Mammary tumor;		
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altshul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Tsohbyki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RN	[2] PREQUENCE FROM N_A.		
RP	SEQUENCE FROM N_A.		
RC	STRAIN=CZECH II; TISSUE=Mammary tumor;		
RA	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.		
RL	RN [3]		
DR	MCD; MGI:2385237; Jtv1; InterPro; IPR00446; GST_C-term.		
DR	InterPro; IPR010987; GST_C-like.		
DR	pFam; PF00043; GST_C; 1;		
SQ	SEQUENCE 320 AA; 35423 MW; 1C21FLA74C98B2B4 CRC64;		
Qy	Query Match Best Local Similarity 87.8%; Score 1464; DB 2; Length 320; Matches 279; Conservative 16; Mismatches 25; Indels 0; Gaps 0;		
Db	1 MPMYQVKYHGGGAPRLVPLPTCMRVLVHLLCERFLVSTVTHSSKTSKVPEPNLICFGEOQNKKQPROD 60		
Qy	61 DILKRLYELKAADVGLSKMIQTPDAADLVNTIQADEPTLTNALDIANSVIGKDYGALK 120		
Db	61 DILKRLYELKAADVGLSKMIQTPDAADLVNTIQADEPTLTNALDIANSVIGKDYGALK 120		
Qy	121 DIVINANASPIPLSLVHLRLLCEHFRVLSTVTHSSKTSKVPEPNLICFGEOQNKKQPROD 180		
Db	121 DIVINANASPIPLSLVHLRLLCEHFRVLSTVTHSSKTSKVPEPNLICFGEOQNKKQPROD 180		
Qy	181 YOLGFTLWKVNKTQMKPSITQMPICSEGNTARFLSLFGOKHNAVNLDSWUDIA 240		

RESULT 5

ID	MCA2	CRIGR	STANDARD;	PRT;	320 AA.
AC	MCA2	CRIGR			
DT	16-OCT-2001	(Rel. 40, Created)			
DT	25-OCT-2004	(Rel. 45, Last sequence update)			
DE	Multisynthetase complex auxiliary component p38.				
OS	Cricetulus griseus (Chinese hamster).				
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; NCBI_TaxID=10029;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	Tissue-Ovary;				
RX	MEDLINE=99056915; PubMed=9878398; DOI=10.1006/jmbi.1998.2316;				
RA	Qveilion S., Robinson J.-C., Berthonneau E., Stalicka M., Mirande M.;				
RT	"Macromolecular assemblage of aminoacyl-tRNA synthetases: identification of protein-protein interactions and characterization of a core protein."				
RT	J. Mol. Biol. 285:183-195(1999).				
CC	-!- FINCTION: probable core protein of the multisynthetase complex that serves as a template for the assembly of the supramolecular structure.				
CC	-!- SUBUNIT: Component of the multisynthetase complex which is comprised of a bifunctional glutaminyl-prolyl-tRNA synthetase, the monospecific isoleucyl, leucyl, glutaminyl, methionyl, lysyl, arginyl, and aspartyl-tRNA synthetases as well as three auxiliary proteins, P18, p48 and p43.				
CC	-!- SIMILARITY: Contains 1 GST-like domain.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
DR	EMBL; AF072727; AAD38422.1; -;				
DR	InterPro; IPR010587; GST_C_like.				
DR	InterPro; IPR000446; GST_Cterm.				
DR	Pfam; PF00033; GST_C; 1;				
KW	protein biosynthesis.				
SQ	SEQUENCE 320 AA; 35433 MW; 6D24B033ABC810A CRC64;				

Query Match Best Local Similarity 86.6%; Score 1444; DB 1; Length 320; Matches 277; Conservative 16; Mismatches 109; Indels 0; Gaps 0;

Query 1 MMVYQVKPYHCGGAPLRLVEPTCMRLPNTPHGRYGRAGMAGQHEENLSQALRSRD 60

Db 1 MPMYQVKSYKGSAPLRLVEPTCMRLPNTPHSKTSPADQHGVOESEPSQALRSRD 60

Query 61 DILKRYELKAVDGSKMKTQPDADLDTNIOADETTLNALDNLSVKGDKYGALK 120

RESULT 6

ID	Q833V2	PRELIMINARY;	PRT;	280 AA.	
AC	Q833V2;				
DT	01-JUN-2002	(TREMBrel. 21, Created)			
DT	01-OCT-2003	(TREMBrel. 21, Last sequence update)			
DR	JV1.				
GN	Name=jtv1;				
OS	Mus musculus (Mouse).				
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=FVB/N; TISSUE=Masmary tumor. C3;				
RX	MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derre F.J.G., Klausner R.D., Collins F.S., Wagner L., Shearn C.M., Schnbler G.D., Altechul S.P., Zeeberg B., Buetow K.H., Schaeffer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong I., Stipletton M., Soerens M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.A., Loqueland N.A., Peters G.J., Abramson R.D., Mullally S.J., Boak S.A., McEvran P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Soderzen E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Snechenko Y., Boutard F.G., Blakesley R.W., Tuchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinichman J.W., Schmutz J., Myers R.M., Butterfield Y.S., Jones S.J., Matra M.A., "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=FVB/N; TISSUE=Masmary tumor. C3;				
RA	Strausberg R.;				
RX	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC024480; AXH24480.1; -;				
DR	MGI; MGI:2382237; JV1.				
DR	InterPro; IPR00046; GST_Cterm.				
DR	InterPro; IPR010587; GST_C_like.				
DR	Pfam; PF00043; GST_C; 1;				
SQ	SEQUENCE 280 AA; 31097 MW; B5B81498983FD2E CRC64;				

Query Match Best Local Similarity 75.6%; Score 1260; DB 2; Length 280; Matches 243; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

Query 45 QERSNLQQLAESRQDILKRYELKAVDGSKMKTQPDADLDTNIOADETTLNALDNLSVKGDKYGALK 104

Db	5	QETSEPSLQALESRQDITKRLYELKAADVGLSKWHTPDAVDNTIQADEPTTLN	64	OY	1	MPMVQVPIYHGGAAPRLVELPTOMYRIPNHGRSYGAPGAGHVOEBSNLQALRSQD	60
OY	105	ALDLNSVIGKDYGALKDVINANPASPPLSLVHLRUCHEFRVLSTVTHSSVKSPEN	164	Db	1	MPMYRMQPYCGG--EIQYDPLTCMRYPRVNH----OAVSENLEODAADPAOALESROE	52
Db	65	TLDLNSVIGKDYGALKDVINANPASPPLSLVHLRUCHEFRVLSTVTHSSVKSPEN	124	OY	61	DILKRLYELKAADVGLSKWHTPDAVDNTIQADEPTTLNADLNSVIGKDYGALK	120
OY	165	LKLCFGEOBKQPRODYLQFTLWKVNPKTQMKFSTOMCPLEGEGNIAFLPSLGOK	224	Db	53	DILKRLYELKAADVGLSKWHTPDAVDNTIQADEPTTLNADLNSVIGKDYGALK	112
Db	125	LKLCFGEOBKQSRHEYQLGFTLWKVNPKTQMKFSTOMCPLEGEGNIAFLPSLGOK	184	OY	121	DIVINANPASPPLSLVHLRUCHEFRVLSTVTHSSVKSPENLILCFGEONKKORQD	180
OY	225	HNAVNATLDSWMDIAFOLKESSKEKAAVPSMSNLGKSPLWLAGNLTVDVUWSV	284	Db	113	DIVINANPASPPLSLVHLRUCHEFRVLSTVTHSSVKSPENLILCFGEONKKORQD	172
Db	185	HNAVTLTLTSDWMDIAMFOLREGSSKERAVERPSMSNLGSPWLVNELTVDVUWSV	244	OY	181	YQIGFTLWKVNPKTQMKFSTOMCPLEGEGNIAFLPSLGOKHNAVNATLDSWMDIA	240
OY	285	LQIGGCSVTVPANVORMRSCENLAPNTALKLK	320	Db	173	YQIGFTLWKDVKPKQMKFSTOMCPLEGEGNIAFLPSLGOKHNAVNATLDSWMDIA	232
Db	245	LQIGGCSVTVPANVORMRSCENLAPNTALKLK	280	OY	241	IFOLKESSKEKAAVPSMSNLGKSPLWLAGNLTVDVUWSVQIGGCSVTVPANQ	300
OY	[1]	SEQUENCE FROM N.A.		Db	233	IFOLKESSKEKAAVPSMSNLGKSPLWLAGNLTVDVUWSVQIGGCSVTVPANQ	291
RN	Q6DK86	PRELIMINARY;	PRT;	OY	301	RWRSRSCENLAPNTALKLK	320
RX	ID Q6DK86			Db	292	KWMSKSCENLASFKSVLRFLK	311
RA	AC Q6DK86;			OY		:	:
DT	25-OCT-2004 (TREMBLREL.	28, Created)		Db			
DT	25-OCT-2004 (TREMBLREL.	28, Last sequence update)		OY			
DE	MCC69221; protein			Db			
GN	Name=MCC69221;			OY			
OS	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).			Db			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			OY			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;			Db			
OC	Xenopoda; Xenopus.			OY			
RP	SEQUENCE FROM N.A.			Db			
RC	TISSUE=Embryo;			OY			
RX	Medline=22388257; PubMed=12477932; DOI=10.1073/pnas.24203899;			Db			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			OY			
RA	Klauber R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,			Db			
RA	Altshul S.F., Zeeberg B.B., Buettow K.H., Schaefer C.F., Bhat N.K.,			OY			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heilek P.,			Db			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			OY			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			Db			
RA	Shapiro R.D., Tsohoni M., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			OY			
RA	Raha S.S., Loqueillano N.A., Peters G.J., Abramson R.D., Mulahay S.J.,			Db			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			OY			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			Db			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			OY			
RA	Fahay J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,			Db			
RA	Whiting M., Young A.C., Shvechanko Y., Bouffard G.G.,			OY			
RA	Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,			Db			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			OY			
RA	Krzywinski M.I., Skalska U., Smalius D.E., Schnurch A., Schein J.E.,			Db			
RA	Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human			OY			
RT	"Generation and initial analysis of more than 15,000 full-length human			Db			
RT	and mouse cDNA sequences."			OY			
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			Db			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			OY			
RN	SEQUENCE FROM N.A.			Db			
RC	TISSUE=Embryo;			OY			
RA	Klein S., Gerhard D.S.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.			Db			
DR	EBML: BC074561; AAH74561.1; -			OY			
DR	InterPro: IPR004046; GST_Cterm.			Db			
DR	InterPro: IPR010887; GST_C_like.			OY			
DR	PFAM: PF00043; GST_C; 1.			Db			
SQ	SEQUENCE 311 AA; D98F27F73C466154 CRC64;			OY			
Query Match	68.7%; Score 1144.5; DB 2; Length 311;			Db			
Best Local Similarity	68.8%; Pred. No. 1; Se-84;			OY			
Matches 220;	Conservative 43; Mismatches 48; Indels 9; Gaps 3;			Db			
RT	Deev. Dyn. 225:384-391(2002).			OY			
RT	Medline=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;			Db			
RA	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.; "Genetic and genomic tools for Xenopus research: the NIH Xenopus			OY			
RT	initiative," Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			Db			
RT	Dyn. 225:384-391(2002).			OY			
[3]				Db			

RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA Klein S., Gerhardt D.S.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 EMBL: BC072178; AAC072178.1; -.
 DR InterPro: IPR004056; GST_C-term.
 DR Pfam: PF00043; GST_C; 1.
 SQ SEQUENCE 311 AA; 3444 MW; D5E8325C18D88751 CRC64;

Query Match Best Local Similarity 69.4%; Score 1139.5; DB 2; Length 311; Matches 221; Conservative 40; Mismatches 50; Indels 9; Gaps 3; Qy 1 MPMYQVKYTHGGAPLRLVPLPTCMYRUPNVHGRSGPAGCHYQBEESNLQLESRQ 60
 Do 1 MPMYRMQPYCGG--EIQVQLPTCMYRULPNVPERAT----AEHQADPAIQALSRQ 52
 Qy 61 DILKRLYELKAADVGLSKMQTTPDADLVNITIQAEPITLTNAIDLNSVLGKDYGALK 120
 Db 53 DILKRLYELKAADVGLSKMQTTPDADLVNITIQAEPITLTNAIDLNSVLGKDYGALK 112
 Qy 121 DIVINANPASPPLSLIVHLILCEHRFLRVSTVHTHSSVSVPUVLNLKCFCGEONKKPROD 180
 Db 113 DIVINANPASPPLSLIVHLILCEHRFLRVSTVHTHSSVSVPUVLNLKCFCGEONKKPROD 180
 Qy 181 YOLGFTLWKNPKTOMKSIQTMCPIEGEGNTARPLFSLFQKHKHAVNATLIDSWDIA 240
 Db 173 YOLGFTLWKNPKTOMKSIQTMCPIEGEGNTARPLFSLFQKHKHAVNATLIDSWDIA 232
 Qy 241 IFOKEGSSKEKAVALVRSNSAIGKSPWMLAGNETLAVDVLWSVQOIGCSVTVPANQ 300
 Db 233 IFOKEGSSKEKAVALVRSNSAIGKSPWMLAGNETLAVDVLWSVQOIGCSVTVPANQ 291
 Qy 301 RWRSCENLAPNTALKLK 320
 Db 292 KMMKSCENLASFKSVLRFLK 311

RESULT 9
 Q7ZYD7 PRELIMINARY; PRT; 311 AA.
 ID Q7ZYD7 DT 01-JUN-2003 (TREMBrel. 24, Created)
 DT 01-MAR-2004 (TREMBrel. 26, Last sequence update)
 DE JTV1-prov protein.
 OS Xenopus laevis (African clawed frog).
 OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]—
 SEQUENCE FROM N.A.
 RP TISSUE=Embryo;
 RX MEDLINE=22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Butow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkinck R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
 RA Dichtchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Sores M.B., Bonaldo M.F., Casavant T.L., Scheretz T.B.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gutarine P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Maden A., Young J.W.C., Shcherbenko Y., Bouffard G.G.,
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalius D.E., Schnurch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;

RESULT 9
 Q7ZYD7 PRELIMINARY; PRT; 311 AA.
 ID Q7ZYD7 DT 01-JUN-2003 (TREMBrel. 24, Created)
 DT 01-MAR-2004 (TREMBrel. 26, Last sequence update)
 DE JTV1-prov protein.
 OS Xenopus laevis (African clawed frog).
 OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;

RESULT 10
 OT73CO PRELIMINARY; PRT; 321 AA.
 ID OT73CO AC OT73CO
 DT 01-OCT-2003 (TREMBrel. 25, Created)
 DT 01-OCT-2003 (TREMBrel. 26, Last sequence update)
 DE Zgc:63976.
 DE ORFArnes-zgc-63976;
 OS Brachydanio rerio (zebrafish) (*Danio rerio*).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinoperygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]—
 SEQUENCE FROM N.A.
 TISSUE=Kidney;
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Butow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hoieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Cabaniss T.L., Scheetz T.E.,
 Brownstein M.J., Usdin T.B., Toshiyuki I., Garnicci P., Prange C.,
 Raha S.S., Logueillo N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Bokas S.A., McBwan P.J., McKernan K.J., Malek J.A., Gunnarath P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
 Villalon D.K., Muñiz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahy J., Helton B., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakely R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzywinski M.I., Skalska U., Smialow D.E., Schnurch A., Schein J.E.,
 Jones S.J., Marrs M.A.;
 "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE:kidney;
 RA Straubberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC053178; DAH53178; -;
 ZFIN: ZDB-GENE-030426-2652; zgc:63976.
 DR InterPro: IPR04046; GST_Ctorm.
 DR InterPro: IPR010987; GST_C_like.
 DR Pfam: PF00043; GST_C; 1_34852 MN: BABF6B951208244A CRC64;
 SQ SBSEQUENCE 321 AA; 34852 MN: BABF6B951208244A CRC64;
 Query Match Best Local Similarity 53.2%; Score 887.5; DB 2; Length 321;
 Matches 184; Conservative 50; Mismatches 76; Indels 21; Gaps 8;
 Qy 1 MPKMQVKPVYHGGGAPRLVELPTCMYRMLPNVHGRSYGPAGPAHVQE-ESNLSQLQESRQ 59
 1 MPKMQVKPVY-SPADITVLDLPTCMYKLPNPHAQ-GASLGEHALQNGEVDPVKALEERQ 56
 Qy 60 DDTIKRKLVELKAANDGLSNIQTQPADLQVNTIQADBPPTLT-----TNADLNSV 111
 57 DEIIRKLYELKATVGLAKNTTBDADLDASTLAH-----TLTHTPDAVIRGTADDD 111
 Db RESULT 12
 Q7KUM5 PRELIMINARY; PRT; 301 AA.
 ID Q7KUM5 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 AC Q7KUM5; DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT CG12304-PB. DE CG12304-PB.
 GN ORFName=CG12304;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriidae; Drosophilidae; Drosophila.
 OX NCBI_TaxID:7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196005; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celtniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scheer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon C., Rogers Y.H., Ballez J.R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Balieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhendari D., Bolshakov S.,
 RA Borková D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Burak D.A., Butler H., Cadie E., Centor A., Chandra I.,
 RA Cherry J.M., Cowley S., Dahlke C., Davenport L.B., Davies P.,
 RA Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 OC NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.

QV 183 LGFTLILKNUPKTOMKESIOTMCPIEGEINARFLFSLFGOKINANAVATL--IDSWNDI 239 DT 25-JAN-2005 (Rel. 46, Last sequence update)
 Db DE PROBABLE multi-synthetase complex auxiliary component p38.
 GN ORFNames=CS12304;
 OS Drosophila melanogaster (Fruit fly).
 OC Enkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 NOptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriidae; Drosophilidae; Drosophila.
 OX NCBI TaxID=727;
 RN [1]
 RP SQUENCE FROM N.A.
 RX STRAIN=Berkeley;
 RX MEDLINE=2019606; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adam M.D., Celinker S.E., Holt R.A., Evans C.A., Cocayne J.D.,
 RA Anatantides P.G., Schorer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Preiffer B.D.,
 RA Wan K.H., Boyle C., Baxter E.G., Heit G., Nelson C.R., Mikles G.L.G.,
 RA Abril J.F., Abgyani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Balley R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhanda D., Bolashov S.,
 RA Borkova D., Botchan M.R., Bouc J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dobson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin R.K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Rosler C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ikegami C.,
 RA Jallal M., Kalush F., Karpen G.H., Ke T., Kennison J.A., Kelchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulpa D., Lalai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.-H., Li Z., Liang Y., Lin X.,
 RA Liu X., Matthei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Markulov G., Milshina N.V., Moarry J., Morris J., Mosherf A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusbern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Punj V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamios I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapelet M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,
 RA Zheng X.H., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP GENOME REANNOTATION.
 RX MEDLINE=2242669; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecny P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Battencourt B.R., Celinker S.E., de Grey A.D.N.J.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.,
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0033.1-RESEARCH0033.22(2002).
 CC -1- SUBUNIT: Component of the multi-synthetase complex which is
 CC comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, the
 CC monospecific isoacyl, leucyl, glutamyl, methionyl, lysyl,
 CC arginyl, and aspartyl-tRNA synthetases as well as three auxiliary
 CC proteins, p18, p48 and p43 (By similarity).
 CC -1- SIMILARITY: Contains 1 GST-like domain.

RESULT 15
 MA2_DROME STANDARD PRT: 334 AA.
 ID MCA2_DROME STANDARD PRT: 334 AA.
 AC QPVRR3;
 DT 16-OCT-2001 (Rel. 40, Created)

Db 300 QR 301
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 302 EK 303

Db 293 EK 294
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 11] SQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RN MEDLINE=2019606; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adam M.D., Celinker S.E., Holt R.A., Evans C.A., Cocayne J.D.,
 RA Anatantides P.G., Schorer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Preiffer B.D.,
 RA Wan K.H., Boyle C., Baxter E.G., Heit G., Nelson C.R., Mikles G.L.G.,
 RA Abril J.F., Abgyani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Balley R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhanda D., Bolashov S.,
 RA Borkova D., Botchan M.R., Bouc J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dobson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin R.K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Rosler C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ikegami C.,
 RA Jallal M., Kalush F., Karpen G.H., Ke T., Kennison J.A., Kelchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulpa D., Lalai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.-H., Li Z., Liang Y., Lin X.,
 RA Liu X., Matthei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Markulov G., Milshina N.V., Moarry J., Morris J., Mosherf A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusbern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Punj V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamios I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapelet M., Strong R., Sun E.,
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 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
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 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP GENOME REANNOTATION.
 RX MEDLINE=2242669; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecny P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Battencourt B.R., Celinker S.E., de Grey A.D.N.J.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.,
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0033.1-RESEARCH0033.22(2002).
 CC -1- FUNCTION: Probable core protein of the multi-synthetase complex
 CC that serves as a template for the assembly of the supramolecular
 CC structure (By similarity).
 CC -1- SUBUNIT: Component of the multi-synthetase complex which is
 CC comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, the
 CC monospecific isoacyl, leucyl, glutamyl, methionyl, lysyl,
 CC arginyl, and aspartyl-tRNA synthetases as well as three auxiliary
 CC proteins, p18, p48 and p43 (By similarity).
 CC -1- SIMILARITY: Contains 1 GST-like domain.

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 CC or send an email to license@ist-sib.ch).
 DR
 DR EMBL; AE003530; AAFA9612.1; -.
 DR FLYBase; FBgn0036515; CG12304;
 DR InterPro; IPR010987; GST_C-like.
 DR InterPro; IPR04046; GST_C-term.
 DR Pfam; PF0043; GST_C; 1.
 KW Protein biosynthesis
 FT DOMAIN 280 327
 FT MW; B68PD70AB3621990F CRC64;
 SEQUENCE 334 AA; 36933

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Query Match 12.9%; Score 214.5; DB 1; Length 334;
Best Local Similarity 25.6%; Pred. No. 5; 2e-09;
Matches 85; Conservative 50; Mismatches 120; Indels 77; Gaps 10;
QY
  18 VELPTCMYRLPNTV---HGRSYGAPARGHGTQEBENLSQLA-
Db 13 IKLUPTCMPLKVKNSLAADSLASGSSTSASTSASTSSCLEANRIDRTGRNATCALDLS 54
QY
  55 -----LESRDPDKLRYELMAAVDGISKMQTTPDADLVNIQADEPT 99
Db 73 IGRQIQIPLKKDTASVAAQRKVQLKQLEKQALQGQIR-----AGLGVG--KIFQHT 123
Db
  100 TLTTNALDLNSVLGKOGALKIVINANPASPPLSLVHLRLLCEHFRVLSTVHHSVK 159
Db 124 TAFQONG-----GLKEVPLQDVWNGHPNFTPYAALKAWNLYTIDKTTFHSTMA 176
QY
  160 SV-----PENLKCPGEQNKKQPRODYQIGFTLWKNVPTQMKPSIQTMCPTEGEVN 212
Db 177 DGPAAREFEANLAKV--PVNPALPK---ISVTLLWKNCITEMISSPTMVPIGEVN 230
QY
  213 TARFLSLFQGKHNAVATL---IDSWDIAIFQLEKGSSEKAAVFRSMMSAIGKSPWL 269
Db 231 TIRYLGRGVPAEYRGSPLONEIDLVLDICVOLCANTHCTQAVANVLDRLOKQYF 290
QY
  270 AGNELTVADVILWSVLOQIGGCSVTPANVQR 301
Db 291 GGSQMSVADGVYSSL-----IRMPAVTEK 315

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Search completed: February 23, 2005, 13:57:11
 Job time : 62.9811 secs

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OM protein - Protein search, using sw model
Run on: February 23, 2005, 13:25:39 ; Search time 70.371 seconds
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Title: US-10-622-817-3
Perfect score: 1667
Sequence: 1 MPMYQVKPYHGGGAPLRLVEL.....RMMRSCENILAPFNTALKLK 320
Searched: 2105692 seqs, 386766381 residues

Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqP1990s:*

2: geneseqP1990B:*

3: geneseqP2000s:*

4: geneseqP2018:*

5: geneseqP2002B:*

6: geneseqP2003as:*

7: geneseqP2003bs:*

8: geneseqP2004B:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1667	100.0	320	7 ADRB5813 Human Pro Ades5813 Human Pro
2	1667	100.0	320	8 ABM80843 Abm80843 Tumour-ab
3	1630	97.8	312	2 ABW25776 Jrrv1_prot
4	1630	97.8	312	8 ADRB6551 1-312 ami
5	1378	82.7	272	7 ADC10204 Human Nov Adc10204 Human Nov
6	1191	71.4	229	8 ADRB6553 84-312 am
7	832	49.9	161	0 ADRB6552 1-161 ami
8	247	14.8	51	5 ABP01502 Human ORF Abp01502 Human ORF
9	214.5	12.9	334	4 ABG23964 Abg23964 Novel hum
10	181	10.9	263	3 ABG23964 Novel hum
11	125.5	7.5	716	3 ADR41411 Arabidops Aag41411 Arabidops
12	125.5	7.5	719	3 AAG41410 Arabidops Aag41410 Arabidops
13	125.5	7.5	748	3 AAG41409 Arabidops Aag41409 Arabidops
14	104	6.2	639	4 ABB62218 Drosophila
15	6.2	1512	4 ABU04349 Mammalian	
16	103	6.2	1512	4 AAM78732 Human pro
17	103	6.2	1550	4 AAM79716 Human pro
18	6.1	201	8 ADR24684 Bacterial	
19	6.1	559	2 AAB10682 Polyhydro	
20	101	6.1	826	4 AAB79740 Corynebac
21	101	6.1	826	4 AAB79989 Corynebac
22	101	6.1	826	4 AAU71908 C. glutam
23	101	6.1	833	4 AAB79739 Corynebac
24	101	6.1	833	4 AAB79988 Corynebac
25	6.1	833	4 AAU71907 C. glutam	

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqP1990s:*

2: geneseqP1990B:*

3: geneseqP2000s:*

4: geneseqP2018:*

5: geneseqP2002B:*

6: geneseqP2003as:*

7: geneseqP2003bs:*

8: geneseqP2004B:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
ADE58613
ID ADE58613 standard; protein; 320 AA.
XX
AC ADE58613;
XX
DT 29-JAN-2004 (first entry)
DE Human Protein Q3155, SEQ ID NO 4489.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; cci; ~
spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
RN WO200316475-A2.
XX
PD 27-FEB-2003.
XX
PP 14-AUG-2002; 2002WO-US025765.
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf, C., D'urso, D., Befort, K., Costigan, M.;
XX
DR WPI; 2003-268312/26.
DR GENBANK; Q13155.

PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
XX
PT Claim 1; Page: 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal

ID	IAW25776	standard; protein; 312 AA.	RESULT 4
AC			ADR8651
XX			ID ADR86551 standard; protein; 312 AA.
XX	19-DEC-1997	(first entry)	XX
DT			ADR86551;
XX			AC
DE	JTV1 protein.		
KW	JTV1; hPMS2; probe; detection; chromosome 7; deletion; mismatch repair gene; hereditary non-polyposis colorectal cancer; homologous recombination.		
KW			
OS	Homo sapiens.		
XX			
PN	W09708312-A1.		
XX			
PD	06-MAR-1997.		
XX			
PP	26-AUG-1996;	96WO-US013598.	
XX			
PR	24-AUG-1995;	95US-0051882.	
XX			
PA	(UYJO) UNIV JOHNS HOPKINS.		
XX			
PT	Vogelstein B, Kinzler KW, Nicolaides NC;		
XX			
DR	WPI; 1997-17926916.		
XX			
PT	Novel chromosome 7 gene, JTV1 - used for detecting chromosome 7 deletions, and PMS2 promoter activity.		
XX			
PS	Claim 5; Fig 2; 31pp; English.		
XX			
CC	This sequence is JTV1 protein and is encoded by DNA isolated from human chromosome 7. The JTV1 coding sequence is located upstream from hPMS2.		
CC	CDNA can be used as probes to detect chromosome 7 deletions involving JTV1. Due to the overlapping promoter regions, deletions of JTV1 would also affect PMS2 (a mismatch repair gene) expression, leading to hereditary non-polyposis colorectal cancer. JTV1 can also be used to assay activity or competence of the PMS2 promoter region, the presence of JTV1 suggesting that the PMS2 promoter is intact. JTV1 sequences can also be used to guide homologous recombination at the PMS2 locus.		
CC	Sequence 312 AA;		
SQ	Query Match 97.8%; Score 1630; DB 2; Length 312; Best Local Similarity 100.0%; Pred. No. 4.3e-63; Mismatches 0; Indels 0; Gaps 0; Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Oy	1 MPMYQVKYHGGCAGPRLVPELPTCMYRPNVGRSGYGPAGSHVQEESNLSQLAESRQD 60 1 MPYQVKYHGGCAGPRLVPELPTCMYRPNVGRSGYGPAGSHVQEESNLSQLAESRQD 60		
Db	61 DIKRLYELKAANDGLSKMIDTADLVNTIQADEPTLTNAIDLNSVLGKDYGALK 120 61 DIKRLYELKAANDGLSKMIDTADLVNTIQADEPTLTNAIDLNSVLGKDYGALK 120		
Oy	61 DIKRLYELKAANDGLSKMIDTADLVNTIQADEPTLTNAIDLNSVLGKDYGALK 120 61 DIKRLYELKAANDGLSKMIDTADLVNTIQADEPTLTNAIDLNSVLGKDYGALK 120		
Db	61 DIKRLYELKAANDGLSKMIDTADLVNTIQADEPTLTNAIDLNSVLGKDYGALK 120 61 DIKRLYELKAANDGLSKMIDTADLVNTIQADEPTLTNAIDLNSVLGKDYGALK 120		
Oy	121 DIVINANPASPPLSLVLRLLCEHFRVLSTVTHSSVKSVPENLLKCFGEONKKQPROD 180 121 DIVINANPASPPLSLVLRLLCEHFRVLSTVTHSSVKSVPENLLKCFGEONKKQPROD 180		
Db	121 DIVINANPASPPLSLVLRLLCEHFRVLSTVTHSSVKSVPENLLKCFGEONKKQPROD 180 121 DIVINANPASPPLSLVLRLLCEHFRVLSTVTHSSVKSVPENLLKCFGEONKKQPROD 180		
Oy	181 YOLGFTLIIWKVNPKTOMKPSIOTMCPIEGEGNITARFLPSLSFGOKHNAVNTLSDWIDIA 240 181 YOLGFTLIIWKVNPKTOMKPSIOTMCPIEGEGNITARFLPSLSFGOKHNAVNTLSDWIDIA 240		
Db	61 DIKRLYELKAANDGLSKMIDTADLVNTIQADEPTLTNAIDLNSVLGKDYGALK 120 61 DIKRLYELKAANDGLSKMIDTADLVNTIQADEPTLTNAIDLNSVLGKDYGALK 120		
Oy	241 IOLKEGSSKEKAVFRENSNSALGKSPMLAGNLTAVDWLNSVLUQIGGSVTVPANQ 300 241 IOLKEGSSKEKAVFRENSNSALGKSPMLAGNLTAVDWLNSVLUQIGGSVTVPANQ 300		
Db	61 DIKRLYELKAANDGLSKMIDTADLVNTIQADEPTLTNAIDLNSVLGKDYGALK 120 61 DIKRLYELKAANDGLSKMIDTADLVNTIQADEPTLTNAIDLNSVLGKDYGALK 120		
Oy	301 RMRSCENLAPF 312 301 RMRSCENLAPF 312		
Db	121 DIVINANPASPPLSLVLRLLCEHFRVLSTVTHSSVKSVPENLLKCFGEONKKQPROD 180 121 DIVINANPASPPLSLVLRLLCEHFRVLSTVTHSSVKSVPENLLKCFGEONKKQPROD 180		

PR 04-JUN-2002; 2002US-00379444.
 XX (CURA-) CURAGEN CORP.
 PA
 XX
 PT Agree ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
 PI Dipippo VA, Edinger SR, Eisen A, Ellerman K, Ganguli RA;
 PI Gärlich VL, Gorman L, Guo X, Heimann JL, Hjalt T, Ji W, Kakuda R;
 PI Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;
 PI Ort T, Padigaru M, Pattrurajan M, Pena CEA, Rastelli L, Rieer DK;
 PI Rotheberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderia SK;
 PI Spytek KA, Stone DU, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
 PI Burgess CB, Lepley DM;
 XX DR WPI; 2003-210149/20.
 XX N-PADB; ADC10203.
 XX PR New isolated NOVX polypeptides and nucleic acid molecules useful for
 PT treating, preventing and diagnosing pathological conditions with NOVX-
 PT associated disorders, such as cancer, obesity, diabetes and inflammatory
 XX or CNS diseases.
 PS
 XX Claim 1, SEQ ID NO 226; 77pp; English.
 CC The invention relates to novel isolated polypeptides, mature form of the
 CC polypeptide, a sequence that is 95% identical to the polypeptide or the
 CC polypeptide comprising one or more conservative substitutions. The NOVX-
 CC polypeptide is useful for treating or preventing a pathology associated
 CC with the polypeptide e.g. disorders associated with aberrant expression
 CC or activity of the polypeptide, such as cancer, diabetes, obesity, and
 CC endocrine, CNS and inflammatory disorders. They can also be used in
 CC various detection and screening assays, chromosome mapping, tissue typing
 CC and predictive medicine. This sequence corresponds to one of the
 XX polypeptides of the invention.
 SQ Sequence 272 AA:
 PR 04-JUN-2002; 2002WO-US017443.
 XX Best Local Similarity 82.7%; Score 1378; DB 7; Length 272;
 PR 04-JUN-2001; 2001US-0295607P.
 PR 04-JUN-2001; 2001US-0295661P.
 PR 06-JUN-2001; 2001US-0296404P.
 PR 06-JUN-2001; 2001US-0296418P.
 PR 07-JUN-2001; 2001US-0296575P.
 PR 11-JUN-2001; 2001US-0297414P.
 PR 12-JUN-2001; 2001US-0297573P.
 PR 12-JUN-2001; 2001US-0297567P.
 PR 14-JUN-2001; 2001US-0297205P.
 PR 15-JUN-2001; 2001US-0298528P.
 PR 18-JUN-2001; 2001US-0299133P.
 PR 19-JUN-2001; 2001US-0299230P.
 PR 21-JUN-2001; 2001US-0299499P.
 PR 22-JUN-2001; 2001US-0300177P.
 PR 26-JUN-2001; 2001US-0300893P.
 PR 28-JUN-2001; 2001US-0301530P.
 PR 03-JUL-2001; 2001US-0302951P.
 PR 31-JUL-2001; 2001US-0308890P.
 PR 14-SEP-2001; 2001US-0324669P.
 PR 03-DEC-2001; 2001US-0337477P.
 PR 14-DEC-2001; 2001US-0341522P.
 PR 21-FEB-2002; 2002US-035856P.
 PR 21-FEB-2002; 2002US-0359122P.
 PR 22-FEB-2002; 2002US-0358978P.
 PR 22-FEB-2002; 2002US-0359034P.
 PR 22-FEB-2002; 2002US-0359035P.
 PR 22-FEB-2002; 2002US-0359121P.
 PR 27-FEB-2002; 2002US-035964P.
 PR 01-MAR-2002; 2002US-0360858P.
 PR 12-MAR-2002; 2002US-0363430P.
 PR 10-APR-2002; 2002US-0371346P.
 PR 10-MAY-2002; 2002US-0379444P.

RESULT 6
 PR 04-JUN-2002; 2002US-00379444.
 XX ADR86553
 ID ADR86553 standard; protein; 229 AA.
 XX
 AC ADR86553;
 XX
 PR 18-NOV-2004 (first entry)
 XX DE 84-312 amino acid sequence of p38/JTV-1 protein.
 XX
 KW p38/JTV-1; Cytostatic; cancer; leukemia; anticancer.

OS Homo sapiens.
 XX PN EP1454628-A2.
 XX PD 08-SEP-2004.
 XX PR 03-MAR-2003; 2003KR-00013058.
 XX PA (UYSE-) UNIV SEOUL NAT IND FOUND.
 XX PI Kim S., Park B.;
 XX DR WPI; 2004-627822/61.
 XX N-PSDB; ADR86550.

XX PT New isolated p38/JTV-1 protein, useful as medicament for treating cancer e.g., stomach, liver, blood, bone, pancreatic, skin, head or neck cancer and cutaneous or intraocular melanoma, as well as for screening new anticancer agents.

XX PS Claim 5; SEQ ID NO 6; 47pp; English.

The present invention relates to an isolated p38/JTV-1 protein for use as medicament. The p38/JTV-1 protein or the pharmaceutical composition is useful as medicament for treating breast cancer, large intestinal cancer, lung cancer, small cell lung cancer, stomach cancer, liver cancer, blood cancer, bone cancer, pancreatic cancer, skin cancer, head or neck cancer, cutaneous or intraocular melanoma, uterine sarcoma, ovarian cancer, rectal cancer, anal cancer, colon cancer, fallopian tube carcinoma, endometrial carcinoma, cervical carcinoma, cervical cancer, vaginal carcinoma, endometrial carcinoma, cervical cancer, vulval cancer, vaginal carcinoma, Hodgkin's disease, esophageal cancer, small intestine cancer, endocrine cancer, thyroid cancer, parathyroid cancer, stomach cancer, liver cancer, bone cancer, pancreatic cancer, skin cancer, head or neck cancer, cutaneous or intraocular melanoma, uterine sarcoma, ovarian cancer, rectal cancer, anal cancer, colon cancer, fallopian tube carcinoma, endometrial carcinoma, cervical cancer, vulval cancer, vaginal carcinoma, Hodgkin's disease, esophageal cancer, small intestine cancer, endocrine cancer, thyroid cancer, parathyroid cancer, adrenal cancer, soft tissue tumour, uterine cancer, penile cancer, prostate cancer, chronic or acute leukaemia, lymphocytic lymphoma, bladder cancer, kidney cancer, ureter cancer, renal cell carcinoma, renal pelvic carcinoma, CNS tumour, primary CNS lymphoma, bone marrow tumour, brain stem nerve gliomas, pituitary adenoma, or their combination. The protein is useful as a target for screening new anticancer agents. The present sequence represents the 84-312 amino acid sequence of p38/JTV-1 protein.

XX SQ Sequence 229 AA;

Query Match 71.4%; Score 1191; DB 8; Length 229;
 Best Local Similarity 100.0%; Pred. No. 7.2e-117; Mismatches 0; Indels 0; Gaps 0;

Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy DADLDVNTIQADEPTLTITNALDLSVIGKDYGALKDIVINANPASPPLSLVHLRLC 143
 Db 1 DADLDVNTIQADEPTLTITNALDLSVIGKDYGALKDIVINANPASPPLSLVHLRLC 60

Qy 144 BFRVFLSTVHHSVSKVSPENILKCFGEQNKKQPRDYQLGFTLKWNPVKIQMKSIQT 203
 Db 61 BFRVFLSTVHHSVSKVSPENILKCFGEQNKKQPRDYQLGFTLKWNPVKIQMKSIQT 120

Qy 204 MCPIEGEGNIAFLPSLFGQKHNANVATLISWUDIAFOLKEGSISKEKAFAVFRSMNAL 263
 Db 121 MCPIEGEGNIAFLPSLFGQKHNANVATLISWUDIAFOLKEGSISKEKAFAVFRSMNAL 180

Qy 264 GKSPWMLAGNELTVDVVLWSVQIQQIGCSVTVPANYVORMMSCLAPP 312
 Db 181 GKSPWMLAGNELTVDVVLWSVQIQQIGCSVTVPANYVORMMSCLAPP 229

RESULT 7
 ADR86552
 ID ADR86552 standard; protein; 161 AA.

XX AC ADR86552;
 XX DT 18-NOV-2004 (first entry)

XX

DE 1-161 amino acid sequence of p38/JTV-1 protein.
 XX KW p38/JTV-1; Cytostatic; cancer; leukemia; anticancer.
 XX OS Homo sapiens.
 XX PN EP1454628-A2.
 XX PD 08-SEP-2004.
 XX PR 03-MAR-2003; 2003KR-00013058.
 XX PA (UYSE-) UNIV SEOUL NAT IND FOUND.
 XX PI Kim S., Park B.;
 XX DR WPI; 2004-627822/61.
 XX N-PSDB; ADR86549.

XX PT New isolated p38/JTV-1 protein, useful as medicament for treating cancer e.g., stomach, liver, blood, bone, pancreatic, skin, head or neck cancer and cutaneous or intraocular melanoma, as well as for screening new anticancer agent.

XX RS Claim 5; SEQ ID NO 5; 47pp; English.

The present invention relates to an isolated p38/JTV-1 protein or the pharmaceutical composition is useful as medicament for treating breast cancer, large intestinal cancer, lung cancer, small cell lung cancer, stomach cancer, liver cancer, bone cancer, pancreatic cancer, skin cancer, head or neck cancer, cutaneous or intraocular melanoma, uterine sarcoma, ovarian cancer, rectal cancer, anal cancer, colon cancer, fallopian tube carcinoma, endometrial carcinoma, cervical cancer, vulval cancer, vaginal carcinoma, Hodgkin's disease, esophageal cancer, small intestine cancer, endocrine cancer, thyroid cancer, parathyroid cancer, adrenal cancer, soft tissue tumour, uterine cancer, penile cancer, prostate cancer, chronic or acute leukaemia, lymphocytic lymphoma, bladder cancer, kidney cancer, ureter cancer, renal cell carcinoma, renal pelvic carcinoma, CNS tumour, primary CNS lymphoma, bone marrow tumour, brain stem nerve gliomas, pituitary adenoma, or their combination. The protein is useful as a target for screening new anticancer agents. The present sequence represents the 1-161 amino acid sequence of p38/JTV-1 protein.

XX SQ Sequence 161 AA;

Query Match 49.9%; Score 832; DB 8; Length 161;
 Best Local Similarity 100.0%; Pred. No. 3.9e-79; Mismatches 0; Indels 0; Gaps 0;

Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMNYQVTPYHGCGAPLVELPTCMYRIPNVHGRSYCPAAGCHVQESTSNLSIQALESRQD 60
 Db 1 MMNYQVTPYHGCGAPLVELPTCMYRIPNVHGRSYCPAAGCHVQESTSNLSIQALESRQD 60

Qy 61 DIKRLYELKAADVGLSKMIDPADDLVNTIOADEPTLTITNALDLSVIGKDYGALK 120
 Db 61 DIKRLYELKAADVGLSKMIDPADDLVNTIOADEPTLTITNALDLSVIGKDYGALK 120

Qy 121 DIVINANPASPPLSLVHLRLICEHFRVLSTVTHSSVKS 161
 Db 121 DIVINANPASPPLSLVHLRLICEHFRVLSTVTHSSVKS 161

XX

RESULT 8
 ABP01502
 ID ABP01502 standard; protein; 51 AA.

XX AC ABP01502;
 XX DT 24-JUN-2002 (first entry)

XX

DE Human ORFX protein sequence SEQ ID NO:2986.

XX

KW

Human;

open reading frame; ORFX; gene therapy; cancer; cirrhosis;

KW

hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;

KW

degenerative disorder; osteoarthritis; neurodegenerative disorder;

KW

cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;

KW

hypertension; hypothyroidism; cholesterol ester storage disease;

KW

immune deficiency; immune disorder; infectious disease;

KW

autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;

KW

myasthenia gravis.

OS Homo sapiens.

XX

WO200192523-A2.

PN

XX

PD 06-DEC-2001.

XX

PR 29-MAY-2001; 2001WO-US010836.

XX

PR 30-MAY-2000; 2000US-0206132P.

XX

PR 29-AUG-2000; 2000US-0228716P.

XX

(CURA-) CURAGEN CORP.

XX

PI Shimkets RA, Leach MD;

XX

WPI; 2002-106309/14.

DR N-PSDB; ABN17254.

XX

PT Novel human polypeptides and polynucleotides useful for diagnosing,

PT preventing and treating cardiovascular disease, neurodegenerative,

PT hyperproliferative disorders and autoimmune disorders.

PS Disclosure; SEQ ID NO 2986; 103pp; English.

The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the Specification)). ABN1762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

Sequence 51 AA;
 Query Match 14.8%; Score 247; DB 5; Length 51;
 Best Local Similarity 96.1%; Pred. No. 4.5e-18; Mismatches 1; Indels 0; Gaps 0;
 Matches 49; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 74 DGLSKMQTDPADLVTNTQADEPTTLTNAALDLSVKGALKDVI 124
 Db 1 DGLSKMHTPDAVLVNLQADEPTLTNADLNSVLGKDGVLDIVI 51
 QY 177 DIGPAREFANLAKV- FVNPAIPK---ISVTLWIKNCHESTEIMISSPPTMVYPYGEVN 212
 Db 160 SV-----PENLJKCGRBQNKKQPRODQQLGFTLWIKNVKPTOMKESIQTMCPLEGEGN 212
 Db 124 TAFQNG----GLKEVFLQDVINGHNFVYALLKNAWRNLTYIDVTFTHSTMA 176
 QY 163 IARLFLSFGQKINAVATL---IDSNWDAIFOLKEGSKEKAAYFRSSMSALGKSPWT 269
 Db 231 IIRYLGRVGPAEYREGSPLCNEBDLWICLVCQRLCNTRHQVAMVRDKRLOQQY 290
 QY 270 AGNLTVDVWLWSVQIGGCSVTPANVQR 301

ID ABB62468 standard; protein; 334 AA.
 XX
 AC ABB62468;
 XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 14196.
 XX KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX PR 23-MAR-2001; 2001WO-US009231.
 XX PR 23-MAR-2000; 2000US-0191637P.
 XX PR 11-JUL-2000; 2000US-00614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR N-PSDB; AB06571.
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
 XX BS Disclosure; SEQ ID NO 14196; 21pp + sequence listing; English.
 XX CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB016176-ABJ3051), expressed DNA sequences (ABL01840-ABL1735) and the encoded proteins (AB5777-AB572072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences
 Sequence 334 AA;

Query Match 12.9%; Score 214.5; DB 4; Length 334;
 Best Local Similarity 25.6%; Pred. No. 2.8e-13; Mismatches 50; Mismatches 120; Indels 77; Gaps 10;
 Matches 85; Conservative 50; Mismatches 120; Indels 77; Gaps 10;

QY 18 VELPTCMYPLKNSIAADSISASGSSTSASTSASISSCKELEANRDIRTRNAATCALDLS 72
 Db 13 IKLPTCMYPLKNSIAADSISASGSSTSASTSASISSCKELEANRDIRTRNAATCALDLS 72
 QY 55 -----LESRODDIKRLYMKAAVGDLSKMIQPDAIDLVTMIIQADEPT 99
 Db 73 LGQIQORLKDPTASAAQBKUQSLBKAQGQIR-----AGLGVCQ--KTFQHT 123
 QY 100 TLTPTMLADLNSVLGALKDVIYNANFASPPSLVTHRILCEHRFLVSLVHTHSSVK 159
 Db 124 TAFQNG----GLKEVFLQDVINGHNFVYALLKNAWRNLTYIDVTFTHSTMA 176
 QY 160 SV-----PENLJKCGRBQNKKQPRODQQLGFTLWIKNVKPTOMKESIQTMCPLEGEGN 212
 Db 177 DIGPAREFANLAKV- FVNPAIPK---ISVTLWIKNCHESTEIMISSPPTMVYPYGEVN 230
 QY 213 IARLFLSFGQKINAVATL---IDSNWDAIFOLKEGSKEKAAYFRSSMSALGKSPWT 269
 Db 231 IIRYLGRVGPAEYREGSPLCNEBDLWICLVCQRLCNTRHQVAMVRDKRLOQQY 290
 QY 270 AGNLTVDVWLWSVQIGGCSVTPANVQR 301

RESULT 9

ABB62468

Run on: February 23, 2005, 13:36:20 ; Search time 17.81 Seconds
 OM protein - protein search, using sw mode.

Title:	US-10-622-817-3
Perfect score:	1677
Sequence:	MPMYQVKPVGCGAPRLVELR.....RMRSCENLAPPFNTALKLK 320
Scoring table:	BLOSSUM62
Gappp:	10.0 , Gapext: 0.5
Searched:	513545 seqb, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Issued Patents Al:*

- 1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/POTUS-COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfTies1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1667	100.0	341	4	US-09-949-016-11312
2	1630	97.8	312	2	US-08-518-862C-2
3	1603	6.2	1512	3	US-09-443-184-48
4	97.5	5.8	559	2	US-09-756-317-10
5	97.5	5.8	559	4	US-09-091-609-4
6	97.5	5.8	5215	3	US-09-105-537-2
7	95.8	5.7	559	4	US-09-821-016-1
8	95.5	5.7	559	4	US-10-259-632-4
9	95.5	5.7	559	4	US-10-266-787-1
10	92.5	2954	4	US-09-150-867-1	
11	91.5	474	4	US-09-248-796A-20321	
12	90.5	359	3	US-09-540-824-2	
13	90.5	5.4	597	1	US-09-399-696-72
14	88.5	100.3	1007	4	US-09-538-092-736
15	88.5	5.3	427	4	US-09-449-016-11178
16	88.5	5.3	724	4	US-09-910-920-62
17	88.5	883	4	US-09-976-239-4	
18	88.5	883	4	US-10-289-779B-2	
19	88.5	5.3	914	4	US-09-975-239-4
20	88.5	5.3	914	4	US-10-289-779B-4
21	86.5	5.2	761	3	US-09-122-710-13
22	86.5	5.2	761	3	US-09-556-273-13
23	86.5	211	4	US-09-328-552-6034	
24	86.5	5.2	351	4	US-08-178-257-6
25	86.5	5.2	471	3	US-09-134-001C-4904
26	86.5	1365	3	US-09-376-330-18	
27	86.5	5.2	5194600-4		

Patent No. 5194600

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RESULT 1

US-09-949-016-11312

Sequence 11312, Application US/09949016
 Patent No. 6912339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIORITY APPLICATION NUMBER: 60/241,725
 PRIORITY FILING DATE: 2000-10-20
 PRIORITY APPLICATION NUMBER: 60/237,768
 PRIORITY FILING DATE: 2000-10-03
 PRIORITY APPLICATION NUMBER: 60/231,498
 PRIORITY FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: BlastSeq for Windows Version 4.0
 SEQ ID NO: 11312
 LENGTH: 341
 TYPE: PRT
 ORGANISM: Human
 US-09-949-016-11312

Query Match Best Local Similarity 100.0%; Score 1667; DB 4; Length 341; Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPMYQVKPVGCGAPRLVELPTCMYRLPWNHGSYGPARGAGHQEEQESNLQALLESRD 60

Db 22 MPYQVKPVGCGAPRLVELPTCMYRLPWNHGSYGPARGAGHQEEQESNLQALLESRD 81

QY 61 DLKRLYELKAANVGLSKMQTDPADLVTNIQADEPTLTNAIDLNLSVIGKDYGALK 120

Db 82 DLKRLYELKAANVGLSKMQTDPADLVTNIQADEPTLTNAIDLNLSVIGKDYGALK 141

QY 121 DIVIANPASPPLSVILVLRLLCHFRLVLTSTVHTHSSVKSVPENLKLCPGEONQKOPRD 180

Db 142 DIVIANPASPPLSVILVLRLLCHFRLVLTSTVHTHSSVKSVPENLKLCPGEONQKOPRD 201

QY 181 YQLGFTLWIKNPVPTQMKESIQTMCPISEGNARFLSLFGQHNANATLDSWIDIA 240

Db 202 YQLGFTLWIKNPVPTQMKESIQTMCPISEGNARFLSLFGQHNANATLDSWIDIA 261

QY 241 IFLQKJEGSKKEKAUVFRSKMSALGKSPWLAGNETVADVLWSVLUQIQQGSTVTPANTQ 300

Db 262 IFLQKJEGSKKEKAUVFRSKMSALGKSPWLAGNETVADVLWSVLUQIQQGSTVTPANTQ 321

301 RWMSCENLAPPFNTALKLK 320

Db 322 RWMRSCENLABFNTALKLK 341

RESULT 3

US-03-441-184-48

; Sequence 49 Application US/09443184A

; Patent No. 637231

; GENERAL INFORMATION:

; APPLICANT: Cunningham, Mary Jane

; APPLICANT: Zweiger, Gary

; APPLICANT: Kaser, Matthew R.

; APPLICANT: Panzer, Scott

; APPLICANT: Seilhamer, Jeffrey J.

; APPLICANT: Yue, Henry

; APPLICANT: Azimai, Yalda

; APPLICANT: Lal, Preeti

; TITLE OF INVENTION: MAMMALIAN TOXICOLOGICAL RESPONSE MARKERS

; CURRENT APPLICATION NUMBER: US/09/443, 184A

; CURRENT FILING DATE: 1999-11-19

; NUMBER OF SEQ ID NOS: 138

; SOFTWARE: PERL Program

; SEQ ID NO 48

; LENGTH: 1512

; TYPE: PRT

; ORGANISM: Homo Sapiens

; NAME/KEY: misc feature

; FEATURE:

; OTHER INFORMATION: Incyte ID No. 6372431 2302721CD1

US-09-443-184-48

Query Match 6.2%; Score 103; DB 3; Length 1512;

Best Local Similarity 22.1%; Pred. No. 0_12; Gaps 9;

Matches 45; Conservative 30; Mismatches 69; Indels 60; Gaps 9;

Qy 124 INANPAPSPPLSVLVRHICERHVLSTVHTHSVKSPENLIKCFGEQNKKPRODQL 183

Db 6 LTVNSGDPPLGAI----LAVERHKDDSI---SVEGKENILH----- 41

Qy 184 GFTLIIWKNPKTONKFSTQTMCPCTEGBCNIAFLRFL---PSLFQOKHNAVATLDSWV 237

Db 42 ---VSENVIFTDV-----NSTIYLRVARTTAGLYGS--NLMEHTBDHWL 82

Qy 238 DIAJFOLKEGSSEKAAVFRNSNALSQALRSRD 292

Db 83 EFSATKL--SSCDSFSTINELNHLCSRITYLVGNSLSADLCWATLK--GNAWQEGL 138

Qy 293 --VIVPANVORNRSCENLAPNT 314

Db 139 KQKKAQPVVKRNGFELAQQAFOQ 162

RESULT 4

US-08-156-317-10

; Sequence 10 Application US/08756317

; Patent No. 5849894

; GENERAL INFORMATION:

; APPLICANT: Clemente, Thomas E.

; APPLICANT: Kishore, Ganesh M.

; APPLICANT: Mitsky, Timothy A.

; APPLICANT: Stark, David M.

; TITLE OF INVENTION: Improved Rhodospirillum Rubrum

; TITLE OF INVENTION: Poly-B-Hydroxyalkonoate Synthase

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: TX

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

RESULT 2
US-08-518-862C-2
; Sequence 2, Application US/08518862C
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Nicolaides, Nicholas C.
; TITLE OF INVENTION: Human JTV1 Gene Overlaps PMS2 Gene
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; COUNTY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/518, 862C
; FILING DATE: 24-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarita A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.49697
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-518-862C-2

Query Match 97.8%; Score 1630; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 3_5e-177; Length 312;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPMYQVKPHGGAPLRLVPLTCMIRLPNHRGYSYGPAGAGHVOQRSNLSQLRSRD 60
Db 1 MPYQVKPHGGAPLRLVPLTCMIRLPNHRGYSYGPAGAGHVOBESNLSQLRSRD 60

Qy 61 DIKRLYELKAAYDGLSKMIDQEPDTTQADLVTNTIQAEPTTITNALDLSVNLKGDKYALK 120
Db 61 DIKRLYELKAAYDGLSKMIDQEPDTTQADLVTNTIQAEPTTITNALDLSVNLKGDKYALK 120

Qy 121 DTYINANPASPPLSLVYLHRICERHVLSTVHTHSVKSPENLIKCRGEQNKKPROD 180
Db 121 DIVINANPASPPLSLVYLHRICERHVLSTVHTHSVKSPENLIKCRGEQNKKPROD 180

Qy 181 YOGLFTIWKNPKTONKFSTQTMCPCTEGBCNIAFLRFL---PSLFQOKHNAVATLDSWVIA 240
Db 181 YOGLFTIWKNPKTONKFSTQTMCPCTEGBCNIAFLRFL---PSLFQOKHNAVATLDSWVIA 240

Qy 241 FOLKGSSSKKAAVFRSMISALGKSPWLANNELTADVWLWSVLIQQIGGSTVPAVQ 300
Db 241 FOLKGSSSKKAAVFRSMISALGKSPWLANNELTADVWLWSVLIQQIGGSTVPAVQ 300

Qy 301 RWMRSCENLABFNTALKLK 312
Db 301 RWMRSCENLABFNTALKLK 312

OM protein - protein search, using SW model
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 4, Appli
Sequence 6, Appli
Sequence 5, Appli
Sequence 13717, A
Sequence 92, Appli
Sequence 90, Appli
Sequence 2, Appli
Sequence 5163, AP
Sequence 2, Appli
Sequence 156, APP
Sequence 58879, A
Sequence 53993, A
Sequence 3001, AP

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OM protein - protein search, using SW model

run on: February 23, 2005, 13:34:50 ; Search time 13.3213 Seconds

(without alignments)

2311.294 Million cell updates/sec

Title: US-10-622-817-3

Sequence: 1 MPMQVQPKHGGAPRLVER.....RMRSCENLAPPNTALKLK 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR-79:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match Length	DB ID	Description	
1	155.5	7.5	T52043	probable glutamate-tRNA ligase (EC 6.1.1.17) [imported] - <i>Arabidopsis thaliana</i> (mouse-ear cress)	
2	111	6.7	T01200	C;Species: <i>Arabidopsis thaliana</i> (mouse-ear cress) C;Accession: T52043 R;DAV, I.S.; Golovkin, M.; Ready, A.S. Bioclin. Biophys. Acta 1399, 219-24, 1998	
3	105.5	6.3	G82441	A;Title: Cloning of the cDNA for glutamyl-tRNA synthetase from <i>Arabidopsis thaliana</i> . A;Reference number: Z24836; MUID:965600; PMID:975600	
4	97.5	5.9	A29036	A;Accession: T52043 A;Status: preliminary; translated from GB/EMBL/DDJB	
5	97.5	5.8	JCS517	A;Molecule type: mRNA A;Residues: 1-719 <DAY> A;Cross-references: UNIPROT:OB2462; EMBL:AF06773; PIDN: AAC36469_1 C;Superfamily: Yeast glutamate-tRNA ligase; glutamine-tRNA ligase homology C;Keywords: ligase	
6	97	5.8	A38604	Query Match 7.5%; Score 125.5; DB 2; Length 719; Best Local Similarity 27.3%; Pred. No. 0/017; Gaps 9; Matches 48; Conservative 26; Mismatches 53; Indels 49;	RESULT 1
7	95	5.8	A74241	QY 128 PSSPPLSVLARLCEBHFRRVSTVWHSRSVSPENILKCGEONKKQPRODYQGLTL 187 Db 10 PESPPPLSVLALSASPV---TIDSAATTVPSFV---PSDGKLN----GATV 55	
8	96	5.8	S70770	QY 188 IWKVNVKQTQMRFSIQMCPIEGEGNARFLSILFGQKHNAVNATLDSWVDIA-IFOLKE 246 Db 56 LIRYV-----GRSARKLDPFYG--NNAFDSSQIDEWVDYASVF--SS 93	
9	94	5.6	B29311	QY 247 GSSEKGAFAVFRMSNSALGKSPWLAGBLTVADVVVLMSVLQQIGGCSTVPANQWR 302 Db 94 GSSEFENAC- GRVDKVLESSTFLVGHSLSIADVAWSALAGTG-----ORW 137	
10	93	5.6	D64391		ALIGNMENTS
11	92	5.5	B85594		
12	92	5.5	F64821		
13	92	5.5	F90743		
14	92	5.5	AE2703		
15	92	5.5	E97485		
16	92	5.5	S72842		
17	92	5.5	AF2338		
18	92	5.5	1206		
19	92	5.5	E87072		
20	91.5	5.5	T14156		
21	91.5	5.5	218		
22	91	5.5	G70513		
23	91	5.5	T42531		
24	90.5	5.4	2280		
25	90.5	5.4	T38906		
26	89.5	5.4	905		
27	89.5	5.4	218		
28	89	5.3	1365		
29	88.5	5.3	2		
			XUFF11		

Rho-type GTPase-ac
conserved hypothetical
glutathione trans
translation elonga
tRNA synthase (pyrc
glutathione trans
methyl-accepting C
translation elonga
multifunctional an
hypothetical prote
CTP synthase (pyrc
glutathione trans
methyl-accepting C
translation elonga
unknown protein 11
MAD1 protein - Yea
hypothetical prote

C;Accession: T52043
R;DAV, I.S.; Golovkin, M.; Ready, A.S.
Bioclin. Biophys. Acta 1399, 219-24, 1998
A;Title: Cloning of the cDNA for glutamyl-tRNA synthetase from *Arabidopsis thaliana*.
A;Reference number: Z24836; MUID:965600; PMID:975600
A;Accession: T52043
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 1-719 <DAY>
A;Cross-references: UNIPROT:OB2462; EMBL:AF06773; PIDN: AAC36469_1
C;Superfamily: Yeast glutamate-tRNA ligase; glutamine-tRNA ligase homology
C;Keywords: ligase

Query Match 7.5%; Score 125.5; DB 2; Length 719;
Best Local Similarity 27.3%; Pred. No. 0/017; Gaps 9;
Matches 48; Conservative 26; Mismatches 53; Indels 49;

QY 128 PSSPPLSVLARLCEBHFRRVSTVWHSRSVSPENILKCGEONKKQPRODYQGLTL 187
Db 10 PESPPPLSVLALSASPV---TIDSAATTVPSFV---PSDGKLN----GATV 55

QY 188 IWKVNVKQTQMRFSIQMCPIEGEGNARFLSILFGQKHNAVNATLDSWVDIA-IFOLKE 246
Db 56 LIRYV-----GRSARKLDPFYG--NNAFDSSQIDEWVDYASVF--SS 93

QY 247 GSSEKGAFAVFRMSNSALGKSPWLAGBLTVADVVVLMSVLQQIGGCSTVPANQWR 302
Db 94 GSSEFENAC- GRVDKVLESSTFLVGHSLSIADVAWSALAGTG-----ORW 137

RESULT 2

T01200

probable glutamate-tRNA ligase (EC 6.1.1.17) F21E10.12 - *Arabidopsis thaliana* (mouse-ear cress)

C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01200
R;Davidson, S.; Rohlfing, T.; David, M.; O'Brian, D.
submitted to the EMBL Data Library, April 1998
A;Description: The sequence of *A. thaliana* F21E10.
A;Reference number: Z14259
A;Accession: T01200
A;Status: translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-728 <DAY>
A;Cross-references: UNIPROT:O65253; EMBL:AF058914; NID:93047074; PID:93047084; GSPDB:GN00000000
C;Experimental source: cultivar Columbia
C;Genetics:

A;Gene: ATSP_F21E10.12
A;Map position: 5
A;Intron: 47/2; 89/3; 141/1; 503/3; 659/3
C;Superfamily: yeast glutamate-tRNA ligase; glutamine-tRNA ligase homology
C;Keywords: aminocycl-tRNA synthetase; ligase; protein biosynthesis
Fv223-49/Domain: glutamine-tRNA ligase homology <EGI>
Query Match 6.7%; Score 111; DB 2; Length 728;
Best Local Similarity 25.9%; Pred. No. 0; 3; Mismatches 53; Indels 58; Gaps 10;
Matches 48; Conservative 26; Mismatches 53; Indels 58; Gaps 10;
Qy 128 PASPPLSIVLHLICRERPVLTSHHSYSKVSPEMLKCFGEONKKOPRQDOLGFI 187
Db 10 PESPPPLSVIVLHLICRERPVLTSHHSYSKVSPEMLKCFGEONKKOPRQDOLGFI 187
Qy 188 IWKWPKTQMKSIQTMCPICEGEGNARFLSLFGOKHNAVNT-----LIDSWWD 238
Db 56 LIRYV-----GRAKKLDPYG---NNAPDSQSVLICINMIDEWD 95
Qy 239 IA-IFQLKEGSSEKKAFAVFRSMNSALGKSPWLAGHETVADVWLWSVLOOIG3CSVTVPA 297
Db 96 YASVF--SSGSBFFENAC--GRDVKYLESTFLVHSLSIADVAIWSALAGTG----- 143
Qy 298 NVQRW 302
Db 144 --QRW 146

RESULT 3
G82441 probable glutathione S-transferase VCA0584 [imported] - *Vibrio cholerae* (strain N1691) s
C;Species: *Vibrio cholerae*
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: G82441
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Judson, D.; Brzuska, M.D.; Vaithianathan, J.; Bass, S.; Qin, H.; Dragoi, I.; Saliars, E.
L; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A;Reference number: A82035; MUID:2046833; PMID:10952301
A;Accession: G82441
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-222 <HEI>
A;Cross-references: UNIPROT:Q9KX05; GB:AE004389; GB:AE003853; NID:99657989; PIDN:AAF9648
C;Genetics:
A;Gene: VCA0584
A;Map position: 2
C;Superfamily: hypothetical protein b2302

Query Match 6.3%; Score 105.5; DB 2; Length 222;
Best Local Similarity 25.7%; Pred. No. 0.17; Mismatches 28; Conservative 22; Indels 21; Gaps 4;
Matches 28; Conservative 22; Mismatches 38; Indels 21; Gaps 4;
Qy 197 MKKSIQTMCPICEGEGNARFLSLFGOKHNAVNTLIDSWWDTIAFOLKEGSSKKAFAV 256
Db 97 LMFOQMGSVGPMMQANV-----FVYFPEKIORA---IDRY-----QKEGRRLF 137
Qy 257 RSMNSALGKSPWLAGNETLVAADVVL--WWSV1QOIGCGSWSVTPANVORMW 303
Db 138 EVNDGQLAQNPIVLAGBYTDIATFPWWR1HEWSG1SIDGLTHLQRWM 186

RESULT 4
A29036 glutathione transferase (EC 2.5.1.18) Yb3 - rat
C;Species: *Rattus norvegicus* (Norway rat)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A29036
R;Abramovitz, M.; Listowsky, I.
J. Biol. Chem., 262, 7770-7773, 1987
A;Title: Selective expression of a unique glutathione S-transferase Yb3 gene in rat brain

A;Reference number: A29036; MUID:87222405; PMID:3584141
A;Accession: A29036
A;Molecule type: mRNA
A;Residues: 1-218 <ABR>
A;Cross-references: UNIPROT:P08009; GB:J02744; NID:9204512; PIDN:AAA41292.1; PID:920451
C;Superfamily: glutathione transferase
C;Keywords: transferase

Query Match 5.8%; Score 97.5; DB 2; Length 218;
Best Local Similarity 25.6%; Pred. No. 0.78; Mismatches 33; Indels 31; Gaps 5;
Matches 33; Conservative 24; Mismatches 41; Indels 31; Gaps 5;
Qy 179 QDVLQGFILWIKWPKTQMKSIQTMCPICEGEGNARFLSLFGOKHNAVNT----- 231
Db 49 EKFKLG--LDFENLP----YLIDESHKTIQSNTAHLRL--GRKHNLGETEERIRV 97
Qy 232 -----LIDSWDIA-----IFOLKEGSSKKAFAVFRSMNSALGKSPWLAGNETLVA 278
Db 98 DILENOMDNMRNMLARYLCLYNPDPEKUPLPGYLEQPGMRLYSEFLGKRPWFAGDKITVVD 157
Qy 279 VVLSVSIQQ 287
Db 158 FIAVDLIER 166

RESULT 5
JC5517 Gu'RNA helicase II binding protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 05-Nov-1999
C;Accession: JC5517
R;Valdez, B.C.; Henning, D.; Perlikay, L.; Busch, R.K.; Busch, H.
Biochem. Biophys. Res. Commun. 234, 335-340, 1997
A;Title: Cloning and characterization of Gu'RNA-II binding protein.
A;Reference number: JC5517; MUID:9720420; PMID:9177271
A;Accession: JC5517
A;Molecule type: mRNA
A;Residues: 1-645 <VAL>
A;Cross-references: Uniprot:U78524; NID:9169606; PIDN:ABA58488.1; PID:9169607
A;Note: it is uncertain whether Met-4 or Met-6 is the initiator
C;Comment: This protein is localized to the nucleus and interacts with Gu'RNA helicase I
C;Keywords: phosphoprotein
F;50-58/Region: nuclear location signal
F;362-374/Region: nucleic acid binding signal
F;65,394,624/Binding site: phosphate (Thr) (covalent) #status predicted
F;7,177,322,412,432,450,461,462,470,614,627/Binding site: phosphate (Ser) (covalent) #st
F;54-197,55-554,592-595,606-609/Region: 4-residue repeats (N-T-S-L)
C;Experimental source: serogroup O1; strain N1691; biotype El Tor
A;Gene: VCA0584
A;Map position: 2

Query Match 5.8%; Score 97.5; DB 2; Length 645;
Best Local Similarity 20.5%; Pred. No. 3.7; Mismatches 79; Conservative 56; Mismatches 129; Indels 121; Gaps 20;
Matches 79; Conservative 56; Mismatches 129; Indels 121; Gaps 20;
Qy 16 LRV-ELPCM-YRLPNVHGRSGPAGHGYQEBESNLQALESERDODDLKRLYELKAV 73
Db 8 LRVSELQTYLGAGRNGRKGKHELLKALHLIKAG---CSAVQMKIKEYLYRRRQK--- 62
Qy 74 DGLSKMQTPDADLVNTIQLQDEPTTLTNALDLNSVIGKDYGALKDVTINANPASPL 133
Db 63 -----IMTP-ADLS1PNWHSSPPMATSFS-----TIPOJYDGHPASPL 102
Qy 134 ---SLL-VLHLICERH-RVLSVTHHSYSKSVP-----ENLKK--CFCRQNIKKQ--- 176
Db 103 LKVSLQPKHELPLHPLTSALHPVHDPIKLUQKLPFYDLDLELIKPTSLASDNQSRFRET 162
Qy 177 -----PRDQYQGFILWIKWPKTQMKSIQ-----TMCPICEGEGNARFLSLFGOKHNAVNT----- 211
Db 163 FAFALP1QVOQOQISSM---DISGTCDFVQVQURFCSETSCQEDBFPPMLCVKNT 219
Qy 212 -----NIARFLSLFGOKHNAVNTLIDSWSV-----DI 239
Db 220 KPCSLPGYLPTKNGVPERKPSRPRINTISLV-----RASITVENTIVWSTABIGRIVSM 274
Qy 240 AIPOLKEGSS-----KEKAFAVFRSMNSALGKSPWLAGNETLVAADVVL-WSVLQQIGGC 291

GenCore version 5.1.6
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On protein - protein search, using sw model

Run on: February 23, 2005, 13:33:04 ; Search time 60.8145 Seconds
2694.512 Million cell updates/sec

Title: US-10-622-817-3
Perfect score: 1667
Sequence: 1 MPMYQVKPYHGGGAPLRYEL.....RWRSCENLAPENTALKLK 320

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : uniprot_03;*

1: uniprot_sprot;*

2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1667	100.0	320	1 MC2_HUMAN
2	1663	99.8	320	2 Q96CZ5
3	1464	87.8	320	2 Q8R010
4	1464	87.8	320	2 Q8R2Y6
5	1444	86.6	320	1 MC2_HUMAN
6	1260	75.6	280	2 Q8R3V2
7	1144.5	68.7	311	2 Q6DK86
8	1139.5	68.4	311	2 Q6INU4
9	1132.5	67.9	311	2 Q7ZYD7
10	887.5	53.2	321	2 Q7T3C0
11	267.5	16.0	340	2 Q7QPA3
12	224	13.4	301	2 Q7KUM5
13	224	13.4	313	2 Q8T060
14	224	13.4	322	2 Q6NRM4
15	214.5	12.9	334	1 MC2_DROME
16	125.5	7.5	719	2 Q83462
17	111	6.7	728	2 Q8P253
18	106.5	6.4	880	2 Q8TTW1
19	106.5	6.4	913	2 Q6DRB3
20	106.5	6.4	913	2 Q6PFO4
21	105.5	6.3	2	Q8R050
22	105	6.3	240	2 Q8TR1
23	105	6.3	1312	1 SYEP_MOUSE
24	105	6.3	1800	2 Q7RA2
25	104.5	6.3	922	2 Q7TEM5
26	104	6.2	661	2 Q9vb85
27	104	6.2	702	2 Q8JHC6
28	104	6.2	841	2 Q8TMQ2
29	103	6.2	328	2 Q86X73
30	103	6.2	869	2 Q6PD57
31	103	6.2	1213	2 Q8FTD2

ALIGNMENTS

RESULT 1			
ID	MCA2_HUMAN	STANDARD;	PRT; 320 AA.
AC	Q13155; Q9PIL2;	Created)	
DT	01-NOV-1997 (Rel. 35)	Last sequence update)	
DT	16-OCT-2001 (Rel. 40,		
DT	05-JUN-2004 (Rel. 44, last annotation update)		
DE	Multisynthetase complex auxiliary component p38 (JTV-1 protein)		
DE	(PR00392).		
GN	Name-JTV1;		
OS	Homo sapiens (Human);		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo;		
OX			
RN			
RP	SEQUENCE FROM N.A.		
RX	Nicolaides N.C., Kinzler K.W., Vogelstein B.:		
RX	"Analysis of the 5' region of PMS2 reveals heterogeneous transcripts and a novel overlapping gene.";		
RT	Genomics 29:329-334(1995).		
RL	[2]		
RN	SEQUENCE FROM N.A.		
RC	TISSUE-Lymph;		
RC	MEIDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klauser R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Bustadt K.H., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schatz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		
RA	Bosak S.A., McBain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Wolley K.C., Hickman K.J., Malek J.A., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Shvchenko K.Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA	Schnarch A., Schein J.E., Jones S.J.M., Marra M.A., Smale D.E.,		
RA	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences";		
RT	deduced by analysis of cDNA clones from human fetal liver.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RN	[3]		
RP	SEQUENCE OF 197-320 FROM N.A.		
RC	TISSUE=Fetal liver;		
RA	Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Ouyang S., Luo L., Bi J.,		
RA	Liu M., He F.,		
RT	"Functional prediction of the coding sequences of 121 new genes		
RT	deduced by analysis of cDNA clones from human fetal liver.";		
RL	Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.		
RN	[4]		

RP INTERACTION WITH FUBP1.
 RX MEDLINE=22716800; PubMed=12819782; DOI=10.1038/ng1182;
 RA Kim M.J., Park B.-J., Kang Y.-S., Kim H.J., Park J.-H., Kang J.W.,
 Lee S.W., Han J.M., Lee H.-W., Kim S.;
 RT "Downregulation of FUSE binding protein and c-myc by tRNA synthetase
 cofactor p38 is required for lung cell differentiation.";
 RL Nat. Genet. 34:330-336(2003).
 CC -!- FUNCTION: Probable core protein of the multisynthetase complex
 that serves as a template for the assembly of the supramolecular
 structure. Mediates ubiquitination of FUBP1 and its degradation by
 the proteasome.
 CC -!- SUBUNIT: Component of the multisynthetase complex which is
 comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, the
 monospecific isoleucyl, leucyl, glutamyl, methionyl, lysyl,
 arginyl, and aspartyl-tRNA synthetases as well as three auxiliary
 proteins, p18, p48 and p43. Binds FUBP1.
 CC -!- SIMILARITY: Contains 1 GST-like domain.
 CC -!- CAUTION: Ref.1 sequence differs from that shown due to a
 frameshift in position 312.

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CC EMBL; U24169; AAC50391.1; ALT FRAME.
 CC EMBL; BC002053; AAH02853.1; --.
 DR EMBL; BC010156; AAH0156.1; --.
 DR EMBL; AF116615; AAF71039.1; --.
 DR H-InvDB; HXK0004460; --.
 DR MIM; 600859; --.
 DR InterPro; IPR010987; GST_C-like.
 DR InterPro; IPR004046; GST_C-term.
 DR Pfam; PF00043; GST_C; 1.
 KW Protein biosynthesis.
 SEQUENCE 320 AA; 35349 MW; F25372B63C12BAB CRC64;

Query Match 100.0%; Score 1667; DB 1; length 320;
 Best Local Similarity 100.0%; Pred. No. 6e-127; Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPMYQVKPHGGGAPRLVPLPTCMYRPLPVHGRSYGPAGAGHVOEESNLSQLAESRQD 60
 1 MPYQVKPHGGGAPRLVPLPTCMYRPLPVHGRSYGPAGAGHVOEESNLSQLAESRQD 60

DR DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 QY 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 QY 181 YOLGFTLTIWKNVKTOMPKFSTQMCPIEGENIARFLPSLGQKHNAVNATLSDWIDIA 240
 181 YOLGFTLTIWKNVKTOMPKFSTQMCPIEGENIARFLPSLGQKHNAVNATLSDWIDIA 240
 QY 241 IFOLKEGSSEKKEKAFAVFSMNNSALGKSPWLAGNETLADVLWSVQIQIGCSVTVPANQ 300
 DR 241 IFOLKEGSSEKKEKAFAVFSMNNSALGKSPWLAGNETLADVLWSVQIQIGCSVTVPANQ 300
 301 RWMRSCENLAPENTALKLK 320
 DR 301 RWMRSCENLAPENTALKLK 320

RESULT 2
 Q96C25 PRELIMINARY; PRT; 320 AA.
 ID Q96C25
 AC Q96C25;

DT 01-DEC-2001 (TREMBREL: 19, Created)
 DT 01-DEC-2001 (TREMBREL: 19, Last sequence update)
 DT 01-MAR-2004 (TREMBREL: 26, Last annotation update)
 DE JTVI.
 DE Name=jTVI;
 OS Homo sapiens (Human).
 OC Buker-Yoda; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mamalia; Euthereria; Primates; Catarhini; Hominoidea; Homo.
 OX NCBI_TaxId=9606;
 RN [1].

RP SEQUENCE FROM N.A.
 TISSUE=Placenta;
 RX MEDLINE=2230827; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sheinman C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heleb F.,
 RA Blatchko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Saplakos M., Soares M.B., Borodalo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshimura K., Carninci P., Prange C.,
 RA Raha S.S., Loquaiello P.N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwain J.P., McKernan K.J., Malek J.A., Gunnarsson P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton D., Kettlemen J., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.B., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smilus D.E., Schmrich A., Schonin J.E.,
 RA Jones S.J., Marrs M.A.; "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2].

RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Strausberg R.;
 RL Submitted (SRP-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC013630; AAH1630.1; --.
 DR InterPro; IPR004046; GST_C-term.
 DR InterPro; IPR010987; GST_C-like.
 DR Pfam; PF00043; GST_C; 1.
 SEQUENCE 320 AA; 35335 MW; 1F14BF58612E08 CRC64;

Query Match 99.0%; Score 1663; DB 2; Length 320;
 Best Local Similarity 99.7%; Pred. No. 1.3e-126; Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPYQVKPHGGGAPRLVPLPTCMYRPLPVHGRSYGPAGAGHVOEESNLSQLAESRQD 60
 1 MPYQVKPHGGGAPRLVPLPTCMYRPLPVHGRSYGPAGAGHVOEESNLSQLAESRQD 60

DR DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 QY 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
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 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
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 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
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 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
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 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
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 DR 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
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 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
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 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
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 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
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 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
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 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
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 DR 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
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 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 121 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 61 DILKRYELKAADVGLSKMQTPADLVNTIQADEPTTLTNAIDLNSVIGDKYGALK 120
 1 DIVINANPASPLSVLVRLLCEHFRVSTVTHSSVSKSPENLKKCFGEONKKQPROD 180
 DR 121 DIVINANPASPLSVL

Db	121 DIVINANFASPPPLSLVLHLRLCERYRLVSTVTHSSVKVNPFENLTKFCFGQRKSRHE	180	
Qy	181 YOLGFLLIWKVNPKTOMKFSTOMCPICPIEGNRNARFLSLEQKRNHNAVNTLIDSWDIA	240	
Db	181 YOLGFLLIWKVNPKTOMKFSTOMCPICPIEGNRNARFLSLEQKRNHNAVNTLIDSWDIA	240	
Qy	241 IFOLKEGSSEKAVFRSMNSALGKSPWLAGNEITVADVVLWSVUQIGCGSVTPANVQ	300	
Db	241 MFOLREGSSSEKAVFRSMNSALGKSPWLVGNELTVADVVLWSVUQIGCGSVTPANVQ	300	
Qy	301 RWMRSCNLAPNTALKLK 320		
Db	301 RWLKSCENLAPFSTALQLIK 320		
RESULT 5			
ID	MCA2 CRIGR	STANDARD;	
AC	MCA2 CRIGR	PRT;	320 AA.
DT	16-OCT-2001 (Rel. 40, last sequence update)		
DT	16-OCT-2001 (Rel. 45, last annotation update)		
DB	Multisynthetase complex auxiliary component p38.		
OS	Cricetulus griseus (Chinese hamster).		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus.		
OX	NCBI_TaxID=10029;		
RN	[1] R.P. SEQUENCE FROM N.A..		
RP	TISSUE=ovary;		
RC	Medline:9969915; PubMed=978398; DOI=10.1006/jmbi.1998.2316;		
RA	Querville S., Robinson J.-C., Berthonneau E., Siapecka M., Mirande M.;		
RT	"Macromolecular assembly of aminoacyl-tRNA synthetases: identification of protein-protein interactions and characterization of a core protein." J. Mol. Biol. 285:183-195 (1999).		
-i	FUNCTION: Probable core protein of the multisynthetase complex that serves as a template for the assembly of the supramolecular structure.		
-i	SIMILARITY: Component of the multisynthetase complex which is comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, the nonspecific isoleucyl, leucyl, glutamyl, methionyl, lysyl, arginyl, and aspartyl-tRNA synthetases as well as three auxiliary proteins, p18, p48 and p43.		
-i	SIMILARITY: Contains 1 GST-like domain.		

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EMBL; AF072727; ARD38422.1; -;			
InterPro; IPR01987; GST_C-like.			
InterPro; IPR004046; GST_Cterm.			
Pfam; PF00043; GST_C; 1.			
Protein biosynthesis.			
SEQUENCE 320 AA; 35433 MW; 6D24E033ABC810A CRC64;			
Query Match 86.6%; Score 1444; DB 1; Length 320;			
Best Local Similarity 86.6%; Pred. No. 7_6e-109; Mismatches 27; Indels 0; Gaps 0;			
Matches 277; Conservative 16; Mismatches 27; Indels 0; Gaps 0;			
Y 1 MPMYQVKPHGGGAPRLVPELPTMYRPNHRSYGPAGAHQWESNSLQALESRD 60			
b 1 MPMYQVKPHGGGAPRLVPELPTMYRPNHRSYGPAGAHQWESNSLQALESRD 60			
61 DILKRLYHLKAAYDGLSRMIVQPADIDVNTIQAQDPTTITNALDMSVLGDYGAATK 120			

RESULT 6			
ID	Q8R3V2	PRELIMINARY;	
AC	Q8R3V2;	PRT;	280 AA.
DT	01-JUN-2002 (Tremblrel. 21, Created)		
DT	01-OCT-2003 (Tremblrel. 25, Last sequence update)		
DR	Name=Jtv1;		
OX	Mus musculus (Mouse).		
OS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;		
RN	[1] R.P. SEQUENCE FROM N.A..		
RT	STRAINE-FVB/N; TISSUE= Mammary tumor. C3; MEDLINE=2288257; PubMed=12479732; DOI=10.1073/pnas.242603899; Straubinger R.L., Feingold E.A., Grouse L.H., Dege J.G., Klausner R.D., Collins F.S., Wagner L., Shamien C.M., Schuler G.D., Altshull S.F., Zeeberg B., Bluetow K.H., Schaefer C.F., Blat N.K., Hopkins R.F., Johnson H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.R., Rubin G.M., Hong T., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Budin T.B., Toshikazu S., Carninci P., Prange C., RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mulahay S.J., RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratino P.H., RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Fahay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., RA Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G., RA Blackesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., RA Krzywinski M.I., Skalska U., Smialius D.E., Schnarch A., Schein J.E., RA Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). RA RN [2] R.P. SEQUENCE FROM N.A.. STRAIN=FVB/N; TISSUE=Mammary tumor. C3; RA STRAIN=FVB/N; TISSUE=Mammary tumor. C3; RA Strausberg R.; Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases. DR EML; BC024480; AAH24480.1; -. DR MGII; MGII; 2385237; JTV1. DR InterPro; IPR004046; GST_Cterm. DR InterPro; IPR01987; GST_C-like. DR Pfam; PF00043; GST_C; 1. DR Pfam; PF00043; GST_C; 1. SQ SEQUENCE 280 AA; 31097 MW; E5B8B1498983ED2E CRC64;		
Query Match 75.6%; Score 1260; DB 2; Length 280;			
Best Local Similarity 88.0%; Pred. No. 5_5e-94; Mismatches 14; Mismatches 19; Indels 0; Gaps 0;			
Matches 243; Conservative 14; Mismatches 19; Indels 0; Gaps 0;			
Y 45 QEBNSLQALESRDQDILKRYHLKAAYDGLSRMIVQPADIDVNTIQAQDPTTITNALDMSVLGDYGAATK 120			

Db 5 QETSEPSLQALESRQQDTIKRLYELKAVDGLSKMIPDADLVNTIQADEPTTLATN 64
 Qy ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 105 ALDINSVLGKDVKALKIVINANPASPLSLVHLRULCERVLSTVHTHSSVKUPEN 164
 Qy ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 65 TIDLNSVLGKDVKALKIVINANPASPLSLVHLRULCERVLSTVHTHSSVKUPEN 124
 Qy ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 165 LKKCFGEONKPKOPRDYOLGFTLIWKNVKPKTOMKFSTOTMCPIEGEGRNARFLSIFGQK 224
 Qy ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 125 LVKCFGEOKRKOSRHEIQLGFTLIWKNVKPKTOMKFSTOTMCPIEGEGRNARFLSIFGQK 184
 Qy ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 225 HRAVNATLIDSMDIAFOLKGSSKKAVERSMNSALGKSPWLAGNLTWADVILWSV 284
 Qy ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 185 HNAVTLTLSDWDIAMFOLKGSSKKAVERSMNSALGKSPWLAGNLTWADVILWSV 244
 Qy ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 285 LQOIGGSVTVPAVORMRSBENALPNTAIKLUK 320
 Qy ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 245 IQLTGESSGAAPTNVQWLKSENLAFTSIALQKLK 280
 Qy ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Result 7
 06DK86 PRELIMINARY; PRT; 311 AA.
 AC 06DK86;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DE MGC69221 protein.
 GN Name=MGC69221;
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 RN NCBI_TaxID=8364;
 RP SEQUENCE FROM N.A.
 TISSUE=Embryo;
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX RA
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Heieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McElhanan K.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.B.,
 RA Jones S.J., Marra M.A., Smailus D.E., Sanger J., Schein J.B.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 TISSUE=Embryo;
 RA Klein S., Gerhard D.S.;
 RA Submitted (JUN 2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC04561; AAH75561.1;
 DR InterPro; IPR004046; GST_Cterm.
 DR InterPro; IPR010987; GST_C_like.
 DR Pfam; PP00043; GST_C; 1.
 SQ SEQUENCE 311 AA; 34480 MW; D9827P73C466154 CRC64;

Query Match 68.7%; Score 114.5%; DB 2; Length 311;
 Best Local Similarity 68.8%; Pred. No. 1.Se-84;
 Matches 220; Conservative 43; Mismatches 48; Indels 9; Gaps 3;
 RN [3]

Db 1 MEMYQVPPHYGGGAPIREVELPTOMYLPNPVHGRSGPAGPAGHVQDEESNLQALESRQD 60
 Qy ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1 MPMYRMQPCGCG--EIQDPLPHCPMYLPNPH----OAVENTEBODAQRPAQLESRQD 52
 Qy ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 61 DILKRLYELKAADVGLSKMIQTPDADLVNTIQADEPTLTNALDLSVGLGDALK 120
 Qy ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 53 DILKRLYELKAADVGLSKMIQTPDADLVNTIQADEPTLTNALDLSVGLGDALK 112
 Qy ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 121 DIVINAMAPASPLSLVHLRUCHEHFRVLSTVHTHSSVKUPENLLKCFGEONKPKQRD 180
 Qy ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 113 DIVINAMPLPPLSLLILHSILCERYQVLSAVRHSSIASIPEPLMKCFGBDQKMRHQ 172
 Qy ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 181 YOLGFTLWIKVKPKTOMKFSTOTMCPIEGEGRNARFLSIFGQK 240
 Qy ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 173 YOLGFTLWIKVKPKTOMKFSTOTMCPIEGEGRNARFLSIFGQK 232
 Qy ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 241 IFQIKESSKEVAVFRSMNSALGKSPWLAGNLTWADVIVMSVLOQIGGSVTPANQ 300
 Qy ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 233 IFOIRECSSKEVAVFRSMNSALGKSPWLAGNLTWADVIVMSVLOQIGGSVTPANQ 291
 Qy ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 301 RMRSRCNTLAPENTALIULK 320
 Qy ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 292 KWMKSCENLASPKSVLFLK 311
 RN [1]
 Result 8
 06INU4 PRELIMINARY; PRT; 311 AA.
 AC 06INU4;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DE MGC80304 protein.
 GN Name=MGC80304;
 OS Xenopus laevis (African clawed frog);
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 RN NCBI_TaxID=8355;
 RP SEQUENCE FROM N.A.
 TISSUE=Ovary;
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX RA
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Heieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McElhanan K.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.B.,
 RA Jones S.J., Marra M.A., Smailus D.E., Sanger J., Schein J.B.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 TISSUE=Ovary;
 RX MEDLINE=22341132; PubMed=12455917; DOI=10.1073/pnas.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Generic and genomic tools for Xenopus research: The NIH Xenopus
 initiative";
 Dev. Dyn. 225:384-391 (2002).
 RL [3]

RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBBJ databases.
 DR EMBL; BC07178; AAH2178.1; -.
 DR InterPro; IPR04046; GST_Cter.
 DR Pfam; PF00043; GST_C; 1.
 SQ SEQUENCE 311 AA; 34424 MW; DS8325C18D88751 CRC64;

Query Match 69.4%; Score 1139.5; DB 2; Length 311;
 Best Local Similarity 69.1%; Pred. No. 3.8e-84; RT
 Matches 221; Conservative 40; Mismatches 50; Indels 9; Gaps 3; [3]
 QY 1 MPMYQVKPFGGGAPLRLVLEPLTCMRLPNVHGRSGPARGAGHVOEBSNLSIQALESRD 60
 Db 1 MPYMRMOPCAGG-EIQVQLPTCMYRPNVHAT-----AENHOADPAIQALERSRD 52
 QY 61 DILKRYLYKAANDGLSKMOTPDADLVNTIQABPPTITNAIDLNSLNLGDKYALK 120
 Db 53 DILKRYLYKAANDGLSKMOTPDADLVNTIQABPPTITNAIDLNSLNLGDKYALK 112
 QY 121 DIVANANPASPPSLVHLRICEHFLVLTSHRSVSKSPENLILKCFCQEQNKQPROD 180
 Db 113 DIVINANPSLPLSLLILHSLICERYQVLSAVHTHSITIPEPLIKCIGDQQLMKPRHE 172
 QY 181 YOLGFTLWKVNPKTOMKFSTQMCPIEGEARNARFLSFQGKQHNAVATLIDSWVIA 240
 Db 173 YOLGFTLWKVDPKQPKMFSTQMCPIEGEARNARFLSFQGKQHNAVATLIDSWVIA 232
 QY 241 IFOLKESKESKEAVFMSNSALGKSPWLAGNETVADVTLWSVIOQIGCSVTVPANQ 300
 Db 233 IFOURGSSKESKEAVFMSNSALGKSPWLAGNETVADVTLWSVIOQIGCSVTVPANQ 291
 QY 301 RMRSCENLAPNTALKLK 320
 Db 292 KWKSCENLAPNTALKLK 311

RESULT 9

Q7ZYD7 PRELIMINARY; PRT; 311 AA.
 ID Q7ZYD7; DT 01-JUN-2003 (TREMBREL. 24, Created)
 AC 07ZYD7; DT 01-JUN-2003 (TREMBREL. 24, Last sequence update)
 DE 01-MAR-2004 (TREMBREL. 26, Last annotation update)
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Amura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 RN NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RC TISSUE=Embryo; MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.; "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.", Dev. Dyn. 225:384-391 (2002). [3]

RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo; Klein S., Strausberg R.; Submitted (JAN-2003) to the EMBL/GenBank/DBBJ databases.
 DR EMBL; BC043832; AAH3832.1; -.
 DR InterPro; IPR04046; GST_Cter.
 DR InterPro; IPR010987; GST_C_like.
 DR Pfam; PF00043; GST_C; 1.
 SQ SEQUENCE 311 AA; 34647 MW; 2F08C9DA60DD63BE CRC64;

Query Match 67.9%; Score 1132.5; DB 2; Length 311;
 Best Local Similarity 69.1%; Pred. No. 1.4e-83; RT
 Matches 221; Conservative 39; Mismatches 51; Indels 9; Gaps 4; [3]
 QY 1 MPYMRMOPCAGG-EIQVQLPTCMYRPNVHAT-----QATSENH-BQADPAIQALERSRD 60
 Db 1 MPYMRMOPCAGG-EIQVQLPTCMYRPNVHAT-----QATSENH-BQADPAIQALERSRD 52
 QY 61 DILKRYLYKAANDGLSKMOTPDADLVNTIQABPPTITNAIDLNSLNLGDKYALK 120
 Db 53 DILKRYLYKAANDGLSKMOTPDADLVNTIQABPPTITNAIDLNSLNLGDKYALK 112
 QY 121 DIVANANPASPPSLVHLRICEHFLVLTSHRSVSKSPENLILKCFCQEQNKQPROD 180
 Db 113 DIVINANPSLPLSLLILHSLICERYQVLSAVHTHSITIPEPLIKCIGDQQLMKPRHE 172
 QY 181 YOLGFTLWKVNPKTOMKFSTQMCPIEGEARNARFLSFQGKQHNAVATLIDSWVIA 240
 Db 173 YOLGFTLWKVDPKQPKMFSTQMCPIEGEARNARFLSFQGKQHNAVATLIDSWVIA 232
 QY 241 IFOLKESKESKEAVFMSNSALGKSPWLAGNETVADVTLWSVIOQIGCSVTVPANQ 300
 Db 233 IFOURGSSKESKEAVFMSNSALGKSPWLAGNETVADVTLWSVIOQIGCSVTVPANQ 291
 QY 301 RMRSCENLAPNTALKLK 320
 Db 292 KWKSCENLAPNTALKLK 311

RESULT 10

Q7T3C0 PRELIMINARY; PRT; 321 AA.
 ID Q7T3C0; DT 01-OCT-2003 (TREMBREL. 25, Created)
 AC 07T3C0; DT 01-OCT-2003 (TREMBREL. 25, Last sequence update)
 DE ZGC:63976.
 OS ORFNAMES=zgc_63976; Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Bakutaria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleoste; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 RN NCBI_TaxID=7955;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney; MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603999;
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Sheinman C.M., Schuler G.D.,
 RA Altshuller S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Blatchenko L., Matsubina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Strelchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Logueillo N.A., Peters G.J., Abramson R.D., Mullay S.J.,
 RA Boga S.A., McBrown P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heitman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimes J.W., Schmutz S., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalius D.E., Schnurch A., Schein J.B.,
 RA Jones S.J., Marras M.A.; "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RT [2]
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RL Strausberg R.; Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC053178; ARH53178; 1; --.
 ZFNT; ZDB-GENE-040426-2; zgc:63976.
 DR InterPro; IPR04046; GST_Cterm.
 DR InterPro; IPR010987; GST_C_like.
 PRAM PFM00043; GST_C; 1; --.
 SQ SEQUENCE 321 AA; GST_C; 34852 MW; BABF6B951208244A CRC64;
 Query Match Best Local Similarity 53.2%; Score 887.5; DB 2; Length 340;
 Matches 184; Conservative 55.6%; Pred. No. 1.e-63; Indels 21; Gaps 8;
 QY 1 MPMYQVQPKPHGGPAPRLRVEPTCMVRPLNVHGRSYGPARPGAGHVO-EESNLQALESRQ 59
 1 MPMYQVQPKV--SPADTIVPLTCMVKLPNVHAQ--GASLGEHALQNGEVDPVTKALERSQ 56
 QY 60 DDITKRLYELKAAYDGLSKMQTDDADDVNTIQDADEPTLT-----TNHDANSV 111
 57 DELRKKLIELKATVDGLAKVTIPDADLDSTLAH-----TLTHTPDAVLRGTDADL 111
 Db RESULT 12
 Q7KUM5 PRELIMINARY; PRT; 301 AA.
 ID Q7KUM5
 AC Q7KUM5; PRELIMINARY; PRT; 301 AA.
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DE CG12304-PB;
 GN ORNAMEs=CG12304;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Epiphydriidae; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-B-2016006; Pubmed=10731132; DOI=10.1126/science.287.5461.2105;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.B., Li P.W., Roeckens R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon C., Worfman Y.H., Blazquez R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Besson K.Y., Benos P.V., Berman B.P., Bhambhani D., Bolshakov S.,
 RA Borstova D., Botchman M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Centner A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., May A.D., Dew I., Dietz S.M.,
 RA Dobson K., Doup L.E., Downes M., Dugan-Rocha S., Dunikov B.C., Dunn P.,
 RA Durbin R.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Rosler C., Gabriele A.E., Gatz N.S., Gelbart W.M., Glaser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris P.,
 RA SEQUENCE FROM N.A.

Qy 183 LGTLIWKVPUKQMKESIQTMPIEGGNIAFLPSLFGQRHNAVATL--IDSVDI 239 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 Qy 180 ISVTLWKNCEHETMISPTPMPYVIGEVNITRYLGRVGPPAEVREYESPCLCNBDLVLDI 239 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 Db 240 A1FOLKEGSSKEKAFAVRSMNSALGKSPWLAGNELTVAADVWWSVLCOIGCSVTVPANV 299 DE Probable multi-synthetase complex auxiliary component p38.
 OS ORFNames=CG12304;
 OC Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephdroioidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196005; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scheer S.E., Li P.W., Hoskins R.A., Gallo R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Woitman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazier R.G., Champine M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.I.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Beau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolhakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cailey S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mayes A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Tocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glaser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houson K.A., Howland T.J., Ibegwam C.,
 RA Jallal M., Karpen G.H., Ke Z., Kenison J.A., Kerchuk R.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulj P., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mileshina N.V., Mobarry C., Morris J., Mosheri A.,
 RA Mount S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacieb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Holland J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Schaefer F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman R., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.",
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP GENOME REANNOTATION.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Milligan G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bertram B.P.,
 RA Bettencourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Ashburner M., Gelberd W.M., Rubin G.M.,
 RA Lewis S.E., Yamada C., Ashburner M., Gelberd W.M., Rubin G.M.,
 RA Lewis S.E., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Milligan G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bertram B.P.,
 RA Bettencourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Ashburner M., Gelberd W.M., Rubin G.M.,
 RA Lewis S.E.,
 RA "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.",
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
 CC - FUNCTION: Probable core protein of the multi-synthetase complex
 CC that serves as a template for the assembly of the supramolecular
 CC structure (By similarity).
 CC - SUBUNIT: Component of the multi-synthetase complex which is
 CC comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, the
 CC monospecific isoleucyl-, leucyl-, glutaminyl-, methionyl-, lysyl-,
 CC arginyl-, and aspartyl-tRNA synthetases as well as three auxiliary
 CC proteins, p18, p48 and p43 (By similarity).
 CC - SIMILARITY: Contains 1 GST-like domain.

RESULT 15
 MCA2_DROME STANDARD; PRT; 334 AA.
 ID MCA2_DROME STANDARD; PRT; 334 AA.
 AC Q9VUR3;
 DT 16-OCT-2001 (Rel. 40, Created)

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 CC
 CC
 DR EMBL; AE003530; AAFR9612.1; -.
 DR INTRABC; CQVUR3; -.
 DR FLYBase; FBgn0036515; CG12304.
 DR InterPro; IPR010987; GST_C_Like.
 DR InterPro; IPR004046; GST_Cterm.
 DR Pfam; PF00043; GST_C; 1.
 KW Protein biosynthesis.
 FT DOMAIN 280 327 GST-like.
 SQ SEQUENCE 334 AA; 36533 MW; B89PD7AE621990F CRC64;
 Query Match 12.9%; Score 214.5; DB 1; Length 334;
 Best Local Similarity 25.6%; Pred. No. 5.2e-09;
 Matches 85; Conservative 25 %; Pairs 50; Mismatches 120; Indels 77; Gaps 10;
 QY 18 VELPTCPTYRLPNV---HGRSYGPAPPAGHVGHQEESNLQAA-----
 QY 13 IKLUPCTCMYPLKVNLSLADSLADSLASGSSTSASTSASTSSCLEANRIDRTGRNATCALDLS 72
 QY 55 -----LESRQDDILKRYELKAADVGDGSKMLOTPDADDVTNIQADEPT 99
 QY 73 LGROIQRLLKKDDFTASVRAQEQTKQLQBELKQLGQR-----AGLGVGCG-KTFQHT 123
 QY 100 TLTINNALDILNSVLGKDYGALKDVTINANPASPPLSLVLRHLICHEFRVISTVHHSVK 159
 QY 124 TAFQNG-----GLKEVPLQDVTINSHPNFTPYALLALKKAWARNLTYIDVKTFTTHSTMA 176
 QY 160 SV-----PENIJKCTGEONKKQPROPDYOLGFTLTIWKNVPTKOMFKSIOTMCPIEGEGN 212
 QY 177 DIGPAAPIRFPEANLAKV--PVNLPALPK---ISVTLIWKNCHETEMISSPTMVYPIGEVN 230
 QY 213 TARPLFLSFLFGOKENAVATL--IDSWNDAIFOLKEGGSSKGKEAAVFRSNSALGKSPWL 269
 QY 231 IIRYLGRVGPABSYVEGSPCLNEIDLVLYDCYOLLRCNTHTQVAMVRUMLDKRLOKQDF 290
 QY 270 AGMELTVADVLWSVIOQIGGCSVTFANVOR 301
 QY 291 GGSMQMSVADGVYSSL-----IRNPATEK 315

Search completed: February 23, 2005, 13:57:12
Job time : 61.9811 secs

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OM protein - protein search, using SW model

Run on: February 23, 2005, 13:25:39 ; Search time 70,371 Seconds

1758.725 Million cell updates/sec

Title: US-10-622-817-5

Perfect score: 1655

Sequence: 1 MPMYQVKPVHGGSAPIRVEL.....RWLKSCENLAPFSTALLQLK 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqDPI1980:*
- 2: geneseqDPI1990:*
- 3: geneseqDPI2000:*
- 4: geneseqDPI2010:*
- 5: geneseqDPI2002:*
- 6: geneseqDPI2003ab:*
- 7: geneseqDPI2003bs:*
- 8: geneseqDPI2004ab:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1			
Result No.	Score	Query Match Length	DB ID
1	1464	88.5	320
2	1464	88.5	320
3	1436	86.8	312
4	1436	86.8	312
5	1232	74.4	272
6	1069	64.6	229
7	735	44.4	161
8	248	15.0	51
9	216.5	13.1	334
10	149	8.9	263
11	126.5	7.6	716
12	126.5	7.6	719
13	126.5	7.6	3 AAG4140
14	106	6.4	1512
15	106	6.4	4 AAM78732
16	106	6.4	1550
17	104	6.3	8 ADN23683
18	102	6.2	1049 ADM67090
19	101.5	6.1	724 AAG655046
20	99	6.0	691 AAU04349
21	98	5.9	243 AAU81518
22	98	5.9	243 ABM5677
23	98	5.9	644 ABJ18952
24	98	5.9	690 AAU34345
25	98	5.9	690 ABM71749

ALIGNMENTS

PR 01-NOV-2001; 2001US-0312147P.			
XX	DT	29-JAN-2004	(first entry)
XX	DE	Human Protein Q31355,	SEQ ID NO 4489.
XX	KW	Human; pain; neuronal tissue; gene therapy;	
KW		spinal segmental nerve injury; chronic constriction injury; CCI;	
KW		spared nerve injury; SNI; Chung.	
XX	OS	Homo sapiens.	
XX	PN	W02003016475-A2.	
XX	PD	27-FEB-2003.	
XX	PP	14-AUG-2002; 2002WO-US025765.	
PR	PR	01-NOV-2001; 2001US-0346302P.	
XX	PR	26-NOV-2001; 2001US-0333347P.	
XX	PA	(GEHO) GEN HOSPITAL CORP.	
XX	PA	(FARB) BAYER AG.	
XX	PI	Woolf, C, D'urso, D, Befort, K, Costigan, M;	
XX	DR	WBT; 2003-268312/26.	
XX	PS	GENBANK; Q13155.	
PT	New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.		
XX	The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal		

ID AAW25776 standard; protein: 312 AA.
 XX
 AC AAW25776;
 XX
 DT 19-DEC-1997 (first entry)
 XX
 DE JTV1 protein.
 XX
 KW JTV1; hPMs2; probe; detection; chromosome 7; deletion; mismatch repair gene; hereditary non-polyposis colorectal cancer; homologous recombination.
 XX
 OS Homo sapiens.
 XX
 PN WO9708312-A1.
 XX
 PD 06-MAR-1997.
 XX
 PP 26-AUG-1996; 96WO-US013598.
 XX
 PR 24-AUG-1995; 95US-00518662.
 XX
 PA (UYJO) UNTV JOHNS HOPKINS.
 XX
 PT vogelstein B, Kinzler KW, Nicolaides NC;
 XX
 PT WPI; 1997-17926916.
 DR N-PSDB; ATB86182.
 XX
 PT Novel chromosome 7 gene, JTV1 - used for detecting chromosome 7 deletions, and PMS2 promoter activity.
 XX
 PS Claim 5; Fig 2; 31pp; English.
 XX
 CC This sequence is JTV1 protein and is encoded by DNA isolated from human chromosome 7. The JTV1 coding sequence is located upstream from hPMs2. JTV1 cDNA can be used as probes to detect chromosome 7 deletions involving JTV1. Due to the overlapping promoter regions, deletions of JTV1 would also affect PMS2 (a mismatch repair gene) expression, leading to hereditary non-polyposis colorectal cancer. JTV1 can also be used to assay activity or competence of the PMS2 promoter region, the presence of JTV1 suggesting that the PMS2 promoter is intact. JTV1 sequences can also be used to guide homologous recombination at the hPMs2 locus
 XX
 SQ Sequence 312 AA;

Query Match 86.8%; Score 1436; DB 2; Length 312;
 Best Local Similarity 87.5%; Pred. No. 5.6e-139;
 Matches 273; Conservative 14; Mismatches 25; Indels 0; Gaps 0;

Oy 1 MPMYQVKPYHGSAPRLVPELPTCMYRPNVHSKTSPATDAGHQVQESPSIQLAESRQD 60
 Db 1 MPMYQVKPYHGGGAPLVELPTCMYRPNVHGRSYGPARGAGHVQESBNLSQALERSQD 60

Oy 61 DILKRLYELKAADVGLSKMIIHPADLVTNIQADEPTTLATNTLDLNSVLGKDYGALK 120
 Db 61 DILKRLYELKAADVGLSKMIIHPADLVTNIQADEPTTLATNTLDLNSVLGKDYGALK 120

Oy 121 DIVINANPASPPLSLVHLRLICERYVLTWTHSSVKNVPEBNLVKGEOARKSRE 180
 Db 121 DIVINANPASPPLSLVHLRLCEHFRVLSTWTHSSVKNVPEBNLVKGEOARKSRE 180

Oy 181 YOLGFTLWKNVKTOMKPSVQCMCPEEGEIGNARFLPSLFGOKHNNAVTLLSDWIDIA 240
 Db 181 YOLGFTLWKNVKTOMKPSVQCMCPIEGEIGNARFLPSLFGOKHNNAVTLLSDWIDIA 240

Oy 241 MFQIREGSSKEKAUFRMSNALSAGRSRPLVGNLTVADWVJNSVLOQTGGSSQAIPINQ 300
 Db 241 IFOLKESSEKKAUFRMSNALSAGRSRPLVGNLTVADWVJNSVLOQTGGCSVTVPANQ 300

Oy 301 RWIKSCENLAFF 312
 Db 301 RWIKSCENLAFF 312

RESULT 4
 XX
 ID ADR86551 standard; protein: 312 AA.
 XX
 AC ADR86551;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE 1-312 amino acid sequence of p38/JTV-1 protein.
 XX
 KW p38/JTV-1; Cytostatic; cancer; leukemia; anticancer.
 XX
 OS Homo sapiens.
 XX
 PN EP1454628-A2.
 XX
 PD 08-SEP-2004.
 XX
 PR 09-SEP-2003; 2003EP-00020344.
 XX
 PR 03-MAR-2003; 2003KR-00013058.
 XX
 PA (UYSE-) UNIV SEOUL NAT IND FOUND.
 XX
 PI Kim S, Park B;
 XX
 DR WPI; 2004-627822/61.
 XX
 PS N-PSDB; ADP86548.
 XX
 PT New isolated p38/JTV-1 protein, useful as medicament for treating cancer e.g., stomach, liver, blood, bone, pancreatic, skin, head or neck cancer
 PT and cutaneous or intraocular melanoma, as well as for screening new PT anticancer agents.
 XX
 PS Claim 5; SEQ ID NO 4; 47PP; English.
 XX
 CC The present invention relates to an isolated p38/JTV-1 protein for use as medicament. The p38/JTV-1 protein or the pharmaceutical composition is useful as medicament for treating breast cancer, large intestinal cancer, lung cancer, small cell lung cancer, stomach cancer, liver cancer, blood cancer, bone cancer, pancreatic cancer, skin cancer, head or neck cancer, rectal cancer, colon cancer, fallopian tube carcinoma, ovarian cancer, endometrial carcinoma, cervical cancer, vulval cancer, vaginal carcinoma, CC Hodgkin's disease, esophageal cancer, small intestine cancer, endocrine cancer, thyroid cancer, parathyroid cancer, adrenal cancer, soft tissue tumour, urethral cancer, penile cancer, prostate cancer, chronic or acute CC leukemia, lymphocytic lymphoma, bladder cancer, kidney cancer, uterine cancer, renal cell carcinoma, renal pelvic carcinoma, CNS tumour, primary CNS lymphoma, bone marrow tumour, brain stem nerve gliomas, pituitary adenoma, or their combination. The protein is useful as a target for screening new anticancer agents. The present sequence represents the 1-312 amino acid sequence of p38/JTV-1 protein.
 CC
 XX
 SQ Sequence 312 AA;

Query Match 86.8%; Score 1436; DB 8; Length 312;
 Best Local Similarity 87.5%; Pred. No. 5.6e-139;
 Matches 273; Conservative 14; Mismatches 25; Indels 0; Gaps 0;

Oy 1 MPMYQVKPYHGSAPRLVPELPTCMYRPNVHSKTSPATDAGHQVQESPSIQLAESRQD 60
 Db 1 MPMYQVKPYHGGGAPLVELPTCMYRPNVHGRSYGPARGAGHVQESBNLSQALERSQD 60

Oy 61 DILKRLYELKAADVGLSKMIIHPADLVTNIQADEPTTLATNTLDLNSVLGKDYGALK 120
 Db 61 DILKRLYELKAADVGLSKMIIHPADLVTNIQADEPTTLATNTLDLNSVLGKDYGALK 120

Oy 121 DIVINANPASPPLSLVHLRLICERYVLTWTHSSVKNVPEBNLVKGEOARKSRE 180
 Db 121 DIVINANPASPPLSLVHLRLCEHFRVLSTWTHSSVKNVPEBNLVKGEOARKSRE 180

Homo sapiens.
 OS DB 1-161 amino acid sequence of p38/JTV-1 protein.
 XX XX
 PN KW p38/JTV-1; Cytostatic; cancer; leukemia; anticancer
 vv vvv

08-SEP-2004.
09-SEP-2003; 2003EP-00020344.

(UYSE-) UNIV SEOUL NAT IND FOUND.
03-MAR-2003; 2003KK-00013058.

KIM S., PARK B;

New isolated p38/JTV-1 protein, useful as medicament for treating cancer e.g., stomach, liver, blood, bone, pancreatic, skin, head or neck cancer and cutaneous or intracocular melanoma, as well as for screening new

Claim 5; SEQ ID NO 6; 47pp; English.

The present invention relates to an isolated p38/JMV-1 protein for use as medicament. The p38/JMV-1 protein or the pharmaceutical composition is useful as a medicament for treating breast cancer, large intestinal cancer, lung cancer, small cell lung cancer, stomach cancer, liver cancer, blood

cancer, bone cancer, pancreatic cancer, skin cancer, head or neck cancer, cutaneous or intracocular melanoma, uterine sarcoma, ovarian cancer, rectal cancer, anal cancer, colon cancer, fallopian tube carcinoma, endometrial carcinoma, cervical cancer, vulval cancer, vaginal carcinoma.

Hodgkin's disease, esophageal cancer, small intestine cancer, endocrine cancer, thyroid cancer, parathyroid cancer, adrenal cancer, soft tissue tumour, urethral cancer, penile cancer, prostate cancer, chronic or acute leukemia, lymphocytic lymphoma, bladder cancer, kidney cancer, uterine

cancer, renal cell carcinoma, renal pelvic carcinoma, CNS tumour, primary CNS lymphoma, bone marrow tumour, brain stem nerve gliomas, pituitary adenoma, or their combination. The protein is useful as a target for screening new anticancer agents. The present sequence represents the 84-

Sequence 229 AA;

every Match 64.6%; Score 1069; DB 8; Length 229;
st Local Similarity 88.2%; Pred. No. 2.6e-101; Mismatches 15; Indels 0; Gaps 0;

84 DADLOVNTILQADEPTTLATNTLIDNSVIGKDYGALKDQIVINANPASPLSLVHLRIC 143
||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 DADLOVNTIQADEPTLTNAIDNSVIGKDYGALKDQIVINANPASPLSLVHLRIC 60

144 ERVVLSTWTHSSVKVNPELJKCFGQARKRSRHEYOLGFPLIWKVUPKTOMKFSQT 203
| : | || | | | | : | | | : | | | | : | | | | | | | | : | | | | | | | | : |
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
61 ERVVLSTWTHSSVKVNPELJKCFGQARKRSRHEYOLGFPLIWKVUPKTOMKFSQT 120

204 MCPIEGEGRNIAREFLSLFGQKHNAVTLTLDSDWUDIAMFQLRGSSKEKA
263
211 MCPIEGEGRNIAREFLSLFGQKHNAVTLTLDSDWUDIAFQLKGSSKEKA
180 VFRMSNAL

264 GRSPWMLVGNELTVADVLMSLQQTGGSGAAPTINORMLKSCLSCENIAPP 312
 :|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 181 GSPWMLVGNELTVADVLMSLQQTGGSGAAPTINORMLKSCLSCENIAPP 229

PRAESIT

ADR86552 standard: protein: 161 AA.

XX
AC
XX
DT
18-NOV-2004 (first entry)
ADR86552;

DE	1-161 amino acid sequence of p38/JTV-1 protein.
XX	p38/JTV-1; Cytostatic; cancer; leukemia; anticancer.
KW	
OS	Homo sapiens.
XX	
PN	EP1454628-A2.
XX	
PD	08-SEP-2004.
XX	
PR	09-SEP-2003; 2003EP-00020344.
XX	
PR	03-MAR-2003; 2003KR-00013058.
XX	
PA	(UISE-) UNIV SEOUL NAT IND FOUND.
XX	
PI	Kim S, Park B;
XX	
WPI; 2004-627822/61.	
DR	N-PDBB; ADR86549.
PT	New isolated p38/JTV-1 protein, useful as medicament for treating cancer e.g., stomach, liver, blood, bone, pancreatic, skin, head or neck cancer and cutaneous or intraocular melanoma, as well as for screening new anticancer agents.
PT	
XX	
PS	Claim 5; SEQ ID NO 5; 47pp; English.
XX	
CC	The present invention relates to an isolated p38/JTV-1 protein for use as medicament. The p38/JTV-1 protein or the pharmaceutical composition is useful as medicament for treating breast cancer, large intestine cancer, lung cancer, small cell lung cancer, stomach cancer, liver cancer, blood cancer, bone cancer, pancreatic cancer, skin cancer, head or neck cancer, cutaneous or intraocular melanoma, uterine sarcoma, ovarian cancer, rectal cancer, anal cancer, colon cancer, fallopian tube carcinoma, endometrial carcinoma, cervical cancer, vulva cancer, vaginal carcinoma, Hodgkin's disease, esophageal cancer, small intestine cancer, endocrine cancer, thyroid cancer, parathyroid cancer, adrenal cancer, soft tissue tumour, urethral cancer, penile cancer, prostate cancer, choriocarcinoma or acute leukaemia, lymphocytic lymphoma, bladder cancer, kidney cancer, ureter cancer, renal cell carcinoma, renal pelvic carcinoma, CNS tumour, primary CNS lymphoma, bone marrow tumour, brain stem nerve glioma, pituitary adenoma, or their combination. The protein is useful as a target for screening new anticancer agents. The present sequence represents the 1-161 amino acid sequence of p38/JTV-1 protein.
CC	
CC	Sequence 161 AA;
SQ	Query Match 44.4%; Score 715; DB 8; Length 161; Best Local Similarity 88.8%; Pred. No. 4.4e-67; Mismatches 143; Conservative 5; Mismatches 13; Indels 0; Gaps 0;
Qy	1 MPMYQVKPRTGGSSAPRLVPELPTCMYRPLWVHSKTSRPTDAGIVQEVSESPSLOALESRQD 60 1 MPMYQVKPRTGGSSAPRLVPELPTCMYRPLWVHSKTSRPTDAGIVQEVSESPSLOALESRQD 60
Db	61 DILKRLYELKAADVGLSKMINTPDADLVTNIOADEPTIATNTLIDNSVLGKGDKYALK 120 61 DILKRLYELKAADVGLSKMINTPDADLVTNIOADEPTIATNTLIDNSVLGKGDKYALK 120
Qy	121 DIVINANPASPPLSLVLLVRLLCRVRVLSVTHSNSKV 161 121 DIVINANPASPPLSLVLLVRLLCRVRVLSVTHSNSKV 161
Db	121 DIVINANPASPPLSLVLLVRLLCRVRVLSVTHSNSKV 161

DE Human ORFX protein sequence SEQ ID NO:2986.

KW Human; open reading frame; ORX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; osteoarthritis; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; myasthenia gravis. XX OS Homo sapiens.

XX PN WO200192523-A2.

XX PD 06-DEC-2001.

XX PR 29-MAY-2001; 2001WO-US010836.

XX PR 30-MAY-2000; 2000US-0206132P.

XX PR 29-AUG-2000; 2000US-0228716P.

PA (CURA-) CURAGEN CORP.

XX PT Shimkets RA, Leach MD;

XX PT WPI; 2002-106308/14.

DR N-PSDB; ABN17254.

PT Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.

XX Disclosure; SEQ ID NO 2986; 1037pp; English.

CC The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN17252 encode the human ORFX proteins given in ABP0010 to ABP1500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester disease, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B.: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Disclosure; SEQ ID NO 2986; 1037pp; English.

CC The present invention describes substantially purified human proteins

(referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN17252 encode the human ORFX proteins given in ABP0010 to ABP1500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester disease, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B.: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Disclosure; SEQ ID NO 14196; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL176-ABL351), expressed DNA sequences (ABL01849-ABL16175) and the encoded proteins (RBB5773-ABY2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 334 AA;

Query Match 13.1%; Score 216.5; DB 4; Length 334;
Best Local Similarity 26.0%; Pred. No. 4.8e-12; Gaps 9;
Matches 86; Conservative 48; Mismatches 12; Indels 73; Gaps 9;

QY 3 MYQVKPYHMGASPLRVPLPTCMYPLKVNLSAADSLASGSSTSASTSASTSSCLEANR ID 57
Db 1 MYELKTL--LPOFDIKUPTCMYPLKVNLSAADSLASGSSTSASTSASTSSCLEANR ID 57

QY 43 -----HVOETSEPSIQALESRQDDILKRYELKAADVGDGSKMHTPD 84

Db 58 RTGRNAATCALDIDSLIGRQIQRLKDPTASVARQERKLQKQLEBLKQLGQIR----- 110

QY 85 ADDVNTNLQADEPPTLTINTDLSVIGKDYGALKDQIVINANPASPLSLVHLRLCE 144
Db 111 AGLGVCGV-KTFOHTTAFQNG-----GLKVEVPLQDVINCHPNFIPYALLKQAWRN 161

QY 145 RYRVLSTWTHASVKNV-----PEVNUKCGEQARKQSRSHEYQGFTLWKVNPKTQ 197

Db 162 LYTFDVKPFTHSMADIGPAAREFEANLAKVVPNLP-----KISVTLLWNCHEM 215

QY 198 KFSVQTMPIEGEHNARFLSLFGOKHNAVLT-----IDSWDIAFMQLRGSSKEKAA 254

Db 216 ISSPMTMVPYIPEGVNIRYLSRVGPABYRVGSGSPCLNEIDLVLDICYQLRCNTHTQVA 275

QY 255 VFRSMNSALGRSPFWLVGNELTVADVWLWVSL 285

ID ABB62468 standard; protein; 334 AA.

XX AC ABB62468;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 14196.

XX KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PR 23-MAR-2001; 2001WO-US009231.

XX PR 23-MAR-2000; 2000US-0191637P.

XX PR 11-JUL-2000; 2000US-00614150.

XX PA (PEKE) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;

XX PT WPI; 2001-656860/75.

DR N-PSDB; ABL06571.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.

XX Disclosure; SEQ ID NO 14196; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL176-ABL351), expressed DNA sequences (ABL01849-ABL16175) and the encoded proteins (RBB5773-ABY2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 334 AA;

Query Match 13.1%; Score 216.5; DB 4; Length 334;

Best Local Similarity 26.0%; Pred. No. 4.8e-12; Gaps 9;

Matches 86; Conservative 48; Mismatches 12; Indels 73; Gaps 9;

Db 111 AGLGVCGV-KTFOHTTAFQNG-----GLKVEVPLQDVINCHPNFIPYALLKQAWRN 161

QY 145 RYRVLSTWTHASVKNV-----PEVNUKCGEQARKQSRSHEYQGFTLWKVNPKTQ 197

Db 162 LYTFDVKPFTHSMADIGPAAREFEANLAKVVPNLP-----KISVTLLWNCHEM 215

QY 198 KFSVQTMPIEGEHNARFLSLFGOKHNAVLT-----IDSWDIAFMQLRGSSKEKAA 254

Db 216 ISSPMTMVPYIPEGVNIRYLSRVGPABYRVGSGSPCLNEIDLVLDICYQLRCNTHTQVA 275

RESULT 9

ABB62468

Run on: February 23, 2005, 13:36:20 ; Search time 17.81 Seconds

Title: OM protein - protein search, using sw model

Perfect score: US-10-622-817-5

Sequence: 1 MPMQVKPVPHGGSAPLRVL. RWLKCSCENLAPFSTALQLK 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/pctodata/liaa/5A__COMB.pep:*
- 2: /cgn2_6/pctodata/liaa/5B__COMB.pep:*
- 3: /cgn2_6/pctodata/liaa/6A__COMB.pep:*
- 4: /cgn2_6/pctodata/liaa/6B__COMB.pep:*
- 5: /cgn2_6/pctodata/liaa/PCTUS COMB.pep:*
- 6: /cgn2_6/pctodata/liaa/backFiles1.pep:*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1464	88.5	341	4 US-09-949-016-11312 Sequence 11312, A
2	1436	86.8	312	2 US-09-851-862-2 Sequence 2, Appl
3	106	6.4	1512	3 US-09-443-18448 Sequence 48, Appl
4	96.5	5.8	1440	3 US-09-352-251-37 Sequence 37, Appl
5	90.5	3.5	359	3 US-09-540-824-2 Sequence 2, Appl
6	90	5.4	559	2 US-08-756-317-10 Sequence 10, Appl
7	90	5.4	559	4 US-09-091-609-4 Sequence 4, Appl
8	90	2954	4	4 US-150-867-1 Sequence 1, Appl
9	90	5.4	5215	3 US-09-105-537-2 Sequence 2, Appl
10	89	5.4	1056	4 US-09-595-684B-29 Sequence 29, Appl
11	89	5.4	1057	3 US-09-541-782-0 Sequence 10, Appl
12	89	5.4	1057	4 US-09-721-820-10 Sequence 10, Appl
13	89	5.4	1057	4 US-10-270-085-10 Sequence 10, Appl
14	89	287	4 US-09-919-7826 Sequence 7826, AP	
15	88	5.3	712	4 US-09-489-039-10736 Sequence 10736, A
16	88	5.3	778	4 US-09-583-110-3930 Sequence 3930, AP
17	88	786	4	4 US-09-107-433-3893 Sequence 3893, AP
18	86.5	5.2	520	4 US-09-248-7964-17644 Sequence 17644, A
19	86.5	5.2	967	4 US-09-540-236-2449 Sequence 2449, AP
20	86	5.2	453	4 US-09-489-039-11461 Sequence 11461, A
21	85.5	5.2	556	4 US-09-130-000-6-6329 Sequence 6329, AP
22	85.5	608	4	4 US-09-284-768A-4 Sequence 4, Appl
23	85.5	657	4	4 US-09-284-768A-7 Sequence 7, Appl
24	85	222	4	4 US-09-248-7964-18146 Sequence 18146, A
25	85	5.1	302	4 US-09-107-532A-6924 Sequence 6924, AP
27	85	5.1	559	4 US-09-512-749-2 Sequence 2, Appl
27	85	1971	4	4 US-09-910-272A-1 Sequence 1, Appl

ALIGNMENTS

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RESULT 1
US-09-949-016-11312
; Sequence 11312, Application US/09949016
; Patent No. 6812239

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11312
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-11312

Query Match Best Local Similarity 89.5%; Score 1464; DB 4; Length 341; Matches 279; Conservative 87.2%; Pred. No. 9e-153; Mismatches 25; Indels 0; Gaps 0;

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QY 61 DILKRLYELKAAGDLSKMTHTPDAVDYNTILQADEPTTLATNTLDNSVLGKDGALK 120
Db 82 DILKRLYELKAAGDLSKMTHTPDAVDYNTILQADEPTTLATNTLDNSVLGKDGALK 141
QY 121 DIVINANPASPPLSLVHLICERYKVLSTVHHSYKVNPEUVKCFEQARIQSRHE 180
Db 142 DIVINANPASPPLSLVHLICERYKVLSTVHHSYKVNPEUVKCFEQARIQSRHE 201
QY 181 YOLGETLIKWNKVKTMQKESVOTMCPIEGSGNIAFLFSLFGQKENAVTLLIDSWNDIA 240
Db 202 YOLGETLIKWNKVKTMQKESVOTMCPIEGSGNIAFLFSLFGQKENAVTLLIDSWNDIA 261
QY 241 MFOLREGSSKEKAAYFRSMNSALGRSPWLVNGELTVADWVLSVUQQTGCGSSGAAPTNVO 300
Db 262 YOLGETLIKWNKVKTMQKESVOTMCPIEGSGNIAFLFSLFGQKENAVTLLIDSWNDIA 321
QY 301 RWLKCSCENLAPFSTALQLK 320

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: February 23, 2005, 13:57:26 ; Search time 50.2443 Seconds
(without alignments)
2084.158 Million cell updates/sec

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scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5
Searched:      1380268 seqs, 327241040 residues
Total number of hits satisfying chosen parameters: 1380268
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%

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Total number of hits satisfying chosen parameters: 1380268
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

14	5.6	456	15	US-10-425-114-63166	Sequence 63166, A
15	5.6	204	15	US-10-369-493-10805	Sequence 10805, A
16	5.6	193	16	US-10-437-965-180124	Sequence 180124,
17	5.5	191	15	US-10-369-493-13717	Sequence 13717, A
18	5.5	191	15	US-10-425-114-42633	Sequence 42633, A
19	5.5	805	15	US-10-424-593-191796	Sequence 191796
20	5.5	1319	16	US-10-437-631-197783	Sequence 197783,
21	5.5	1788	16	US-10-437-963-197780	Sequence 197780,
22	5.5	419	15	US-10-424-593-260387	Sequence 260387,
23	90.5	578	15	US-10-418-861B-32	Sequence 32, App1
24	90.5	661	15	US-10-369-493-2558	Sequence 2558, App
25	90.5	716	15	US-10-369-493-2175	Sequence 2175, App
26	90	559	9	US-09-364-847-21	Sequence 21, App1
27	90	5.4	856	9	US-09-364-847-33
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33	90	5.4	5215	14	US-10-271-889-45
34	90	5.4	203	15	US-10-369-493-8604
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44	88.5	5.3	656	16	US-10-369-493-18559
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SUMMARIES

20: /cgn2_6/pbodata/1/pubpax/us60_PUBCOMB.pep:*

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PRIOR FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4

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1	1436	86.8	312	16	US-0-463-676-4	Sequence 4, APP
2	1069	64.6	229	16	US-10-463-676-6	Sequence 5, APP
3	735	44.4	161	16	US-10-463-676-5	Sequence 6, APP
4	1055	6.4	925	16	US-10-433-963-126132	Sequence 5, APP
5	104	6.3	980	15	US-10-369-493-6336	Sequence 6336, APP
6	1035	6.3	468	15	US-10-424-599-160388	Sequence 260388, APP
7	995	6.0	914	16	US-10-433-993-15870	Sequence 15870, APP
8	99	6.0	691	15	US-10-282-122A-44369	Sequence 44369, APP
9	98	5.9	690	9	US-09-815-442-5841	Sequence 5841, APP
10	96.5	5.8	1440	10	US-03-446-374	Sequence 37, APP
11	96.5	5.8	1440	16	US-10-786-720-31	Sequence 31, APP
12	5.8	569	16	US-10-437-963-123904	Sequence 123904, APP	
13	95	5.7	722	15	US-10-369-493-10013	Sequence 10013, APP

Db 61 DILKRYLEKAVADGLSKMQTPDADTVNIIQADEPTLTINALDINSVLGKDYGALK 120 ; TITLE OF INVENTION: Method for Treating Cancer Using P38/JTV-1 and Method
Qy 121 DIVINANPASPLSLVILVRLLCERYRISVTWTHSSVKVNPENLVICFGEOARKSRSHE 180 ; TITLE OF INVENTION: for Screening Pharmaceutical Composition for Treating Cancer
Db 121 DIVINANPASPLSLVILVRLLCERYRISVTWTHSSVKVNPENLVICFGEOARKSRSHE 180 ; FILE REFERENCE: 01679-091
; CURRENT APPLICATION NUMBER: US/10/463, 676
; CURRENT FILING DATE: 2003-06-18
Qy 181 YOLGFTLWINKVPTKOMKESVQTMCPFEGEGRNARFLSFLFQKHNATLTDWSNDIA 240 ; PRIOR APPLICATION NUMBER: KR 10-2003-13058
Db 181 YOLGFTLWINKVPTKOMKESVQTMCPFEGEGRNARFLSFLFQKHNATLTDWSNDIA 240 ; PRIORITY FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
Qy 241 MFOLRREGSSKEKAAVFRSMNSALGKSPWLAGNLTVADVLSVLSVQIG3CSVTVPANVO 300 ; SEQ ID NO 5
Db 241 MFOLRREGSSKEKAAVFRSMNSALGKSPWLAGNLTVADVLSVLSVQIG3CSVTVPANVO 300 ; LENGTH: 161
; LENGTH: 161
Db 301 RWLKSCENAIAPF 312 ; TYPE: PRY
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(161)
; OTHER INFORMATION: 1-161 amino acid sequence of p38/JTV-1
; US-10-463-676-5
; Query Match
; Best Local Similarity 44.4%; Score 735; DB 16; Length 161;
; Matches 143; Conservative 5; Mismatches 13; Indels 0; Gaps 0;
; Qy 1 MEMWQKPYHGSAPRVEPTCMRLPNHHSKTSPTADAGVQEVSEPSQALERSQRQ 60 ; TITLE OF INVENTION: Method for Treating Cancer Using P38/JTV-1 and Method
; Db 1 MPMYQKPYHGGAPLRLVLPCTMRLPNHGRSYGPAGHVOEERNSLQLAESRQD 60 ; TITLE OF INVENTION: Method for Treating Cancer
; FILE REFERENCE: 012679-091
; CURRENT APPLICATION NUMBER: US/10/463, 676
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: KR 10-2003-13058
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; ORGANISM: Homo sapiens
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; NAME/KEY: PEPTIDE
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Best Local Similarity 88.2%; Pred. No. 4e-100; Mismatches 15; Indels 0; Gaps 0;
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; Query Match 64.6%; Score 1069; DB 16; Length 229;
; Best Local Similarity 88.2%; Pred. No. 4e-100; Mismatches 15; Indels 0; Gaps 0;
; Matches 202; Conservative 12; Mismatches 15; Indels 0; Gaps 0;
; US-10-463-676-6
; RESULT 3
; Sequence 5, Application US/10463676
; Publication No. US20040175375A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Sunghoon
; APPLICANT: Park, Bum-Joon

Db 84 DADIDVNTIQADEPPTLATNTIDLNSTLGKOGALDQIVINANPASPLSLVILVRLLC 143 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
Db 1 DADIDVNTIQADEPPTLATNTIDLNSTLGKOGALDQIVINANPASPLSLVILVRLLC 60 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 3B-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437, 963
; CURRENT FILING DATE: 2003-05-14
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; LENGTH: 925
; Query Match 64.4%; Score 105.5; DB 16; Length 925;
; Best Local Similarity 20.3%; Pred. No. 0.51; Mismatches 107; Indels 99; Gaps 13;
; Matches 64; Conservative 46; Mismatches 107; Indels 99; Gaps 13;
; Type: PRY
; Organism: Oryza sativa
; Feature: Other Information: Oryza sativa
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; US-10-437-963-126132

Db 144 ERYVLSVTHSVKVNPNLYKCFGRQARQSRHYQLOFTLWINKVPTKOMKESVOT 203 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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; US-10-437-963-126132

Db 61 EHKFLVSTVTHSVKVNPNLYKCFGRQARQSRHYQLOFTLWINKVPTKOMKESVOT 120 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/437, 963
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; Organism: Oryza sativa
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; US-10-437-963-126132

Db 204 MCPLEGEMIARLFLSFLFGQKHNAVTTLISWDTAMFOREGSSKEKAAVFRSMNSAL 263 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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; Matches 64; Conservative 46; Mismatches 107; Indels 99; Gaps 13;
; Type: PRY
; Organism: Oryza sativa
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; US-10-437-963-126132

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; US-10-437-963-126132

Db 264 GRPFLVVENETIVADVVLWSWQQTGSSGAAPTAIVORMWIKSCENLA 312 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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; US-10-437-963-126132

Db 181 GKPSPWLAGNELETVADVVLWSVQIQGCGSVTVPANVQRWWSCENLA 229 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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; Type: PRY
; Organism: Oryza sativa
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Db 25 YRLPNVHSKTSPADAGHQETSEPSQALESRQDDI-LKRLYELKAVDGLSKRHT 82 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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; US-10-437-963-126132

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; Feature: Other Information: Oryza sativa
; Other Information: Clone ID: PAT_MRT4530_28709C.1.pep
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Listing first 45 summaries									
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DB									
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Description									

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Bloch, I. Biochemistry. Acta 1399, 219-24, 1998									
A;Title: Cloning of the cDNA for glutamyl-tRNA synthetase from <i>Arabidopsis thaliana</i> .									
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R;Day, I.S.; Golovkin, M.; Reddy, A.S.-									
Bloch, I. Biochemistry. Acta 1399, 219-24, 1998									
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A;Description: The sequence of A. thaliana F21E10.									
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A;Experimental source: cultivar Columbia									
C;Genetics:									

ALIGNMENTS									

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40 89 5.3 2279 2 T45231 acetyl-CoA carboxy	41 88 5.3 2820 2 T3806 ATP-dependent helicase	42 87.5 5.3 474 2 B70597 ATP-dependent helicase	43 87 5.3 820 2 H82022 ATP-dependent helicase	44 87 5.3 570 2 T15163 ATP-dependent helicase	45 86 5.2 906 2 T45158 ATP-dependent helicase	46 86 5.2 906 2 T45158 ATP-dependent helicase	47 86 5.2 906 2 T45158 ATP-dependent helicase	48 86 5.2 906 2 T45158 ATP-dependent helicase	49 86 5.2 906 2 T45158 ATP-dependent helicase
50 86 5.2 906 2 T45158 ATP-dependent helicase	51 86 5.2 906 2 T45158 ATP-dependent helicase	52 86 5.2 906 2 T45158 ATP-dependent helicase	53 86 5.2 906 2 T45158 ATP-dependent helicase	54 86 5.2 906 2 T45158 ATP-dependent helicase	55 86 5.2 906 2 T45158 ATP-dependent helicase	56 86 5.2 906 2 T45158 ATP-dependent helicase	57 86 5.2 906 2 T45158 ATP-dependent helicase	58 86 5.2 906 2 T45158 ATP-dependent helicase	59 86 5.2 906 2 T45158 ATP-dependent helicase
60 86 5.2 906 2 T45158 ATP-dependent helicase	61 86 5.2 906 2 T45158 ATP-dependent helicase	62 86 5.2 906 2 T45158 ATP-dependent helicase	63 86 5.2 906 2 T45158 ATP-dependent helicase	64 86 5.2 906 2 T45158 ATP-dependent helicase	65 86 5.2 906 2 T45158 ATP-dependent helicase	66 86 5.2 906 2 T45158 ATP-dependent helicase	67 86 5.2 906 2 T45158 ATP-dependent helicase	68 86 5.2 906 2 T45158 ATP-dependent helicase	69 86 5.2 906 2 T45158 ATP-dependent helicase
70 86 5.2 906 2 T45158 ATP-dependent helicase	71 86 5.2 906 2 T45158 ATP-dependent helicase	72 86 5.2 906 2 T45158 ATP-dependent helicase	73 86 5.2 906 2 T45158 ATP-dependent helicase	74 86 5.2 906 2 T45158 ATP-dependent helicase	75 86 5.2 906 2 T45158 ATP-dependent helicase	76 86 5.2 906 2 T45158 ATP-dependent helicase	77 86 5.2 906 2 T45158 ATP-dependent helicase	78 86 5.2 906 2 T45158 ATP-dependent helicase	79 86 5.2 906 2 T45158 ATP-dependent helicase
80 86 5.2 906 2 T45158 ATP-dependent helicase	81 86 5.2 906 2 T45158 ATP-dependent helicase	82 86 5.2 906 2 T45158 ATP-dependent helicase	83 86 5.2 906 2 T45158 ATP-dependent helicase	84 86 5.2 906 2 T45158 ATP-dependent helicase	85 86 5.2 906 2 T45158 ATP-dependent helicase	86 86 5.2 906 2 T45158 ATP-dependent helicase	87 86 5.2 906 2 T45158 ATP-dependent helicase	88 86 5.2 906 2 T45158 ATP-dependent helicase	89 86 5.2 906 2 T45158 ATP-dependent helicase
90 86 5.2 906 2 T45158 ATP-dependent helicase	91 86 5.2 906 2 T45158 ATP-dependent helicase	92 86 5.2 906 2 T45158 ATP-dependent helicase	93 86 5.2 906 2 T45158 ATP-dependent helicase	94 86 5.2 906 2 T45158 ATP-dependent helicase	95 86 5.2 906 2 T45158 ATP-dependent helicase	96 86 5.2 906 2 T45158 ATP-dependent helicase	97 86 5.2 906 2 T45158 ATP-dependent helicase	98 86 5.2 906 2 T45158 ATP-dependent helicase	99 86 5.2 906 2 T45158 ATP-dependent helicase
100 86 5.2 906 2 T45158 ATP-dependent helicase	101 86 5.2 906 2 T45158 ATP-dependent helicase	102 86 5.2 906 2 T45158 ATP-dependent helicase	103 86 5.2 906 2 T45158 ATP-dependent helicase	104 86 5.2 906 2 T45158 ATP-dependent helicase	105 86 5.2 906 2 T45158 ATP-dependent helicase	106 86 5.2 906 2 T45158 ATP-dependent helicase	107 86 5.2 906 2 T45158 ATP-dependent helicase	108 86 5.2 906 2 T45158 ATP-dependent helicase	109 86 5.2 906 2 T45158 ATP-dependent helicase
110 86 5.2 906 2 T45158 ATP-dependent helicase	111 86 5.2 906 2 T45158 ATP-dependent helicase	112 86 5.2 906 2 T45158 ATP-dependent helicase	113 86 5.2 906 2 T45158 ATP-dependent helicase	114 86 5.2 906 2 T45158 ATP-dependent helicase	115 86 5.2 906 2 T45158 ATP-dependent helicase	116 86 5.2 906 2 T45158 ATP-dependent helicase	117 86 5.2 906 2 T45158 ATP-dependent helicase	118 86 5.2 906 2 T45158 ATP-dependent helicase	119 86 5.2 906 2 T45158 ATP-dependent helicase
120 86 5.2 906 2 T45158 ATP-dependent helicase	121 86 5.2 906 2 T45158 ATP-dependent helicase	122 86 5.2 906 2 T45158 ATP-dependent helicase	123 86 5.2 906 2 T45158 ATP-dependent helicase	124 86 5.2 906 2 T45158 ATP-dependent helicase	125 86 5.2 906 2 T45158 ATP-dependent helicase	126 86 5.2 906 2 T45158 ATP-dependent helicase	127 86 5.2 906 2 T45158 ATP-dependent helicase	128 86 5.2 906 2 T45158 ATP-dependent helicase	129 86 5.2

A;Gene: ATSPF21E10.12
A;Map position: 5
A;Introns: 47/2; 89/3; 141/1; 503/3; 659/3
C;Superfamily: Yeast glutamate-tRNA ligase; glutamine-tRNA ligase homology
C;Keywords: aminoacyl-tRNA synthetases; ligase; protein biosynthesis
F.223-499/Domain: glutamine-tRNA ligase homology <BGL>

Query Match 6.8%; Score 112; DB 2; Length 728;
Best Local Similarity 26.6%; Pred. No. 0..29; Mismatches 49; Conservative 22; Indels 56; Gaps 9; Matches 49; Conservative 22; Mismatches 57; Indels 56; Gaps 9;

Qy 128 PASPPLSILVILRLCERYRVISVTHSSVKVNPENLWKCFGEQARKKSRHEYQIGFTI 187
Db 10 PESPPPLSVIVALSLSASPV---TIDSSAAATTVPFSFV---SGRKLN-----GATV 55
Qy 188 IWKWPKTQMKRSVQTMCPIEGEGNARFLFSLFGOKRNHATLT-----LIDSWD 238
Db 56 LIRYV-----GRSAKKLFDYG--NNADSSQSVSILCINMKIDEWD 95
Qy 239 IAMFOREGSSKEKAAVFRSNSALGRSPMIVGNELTVAQVVLNSVLODGSSGAAPIN 298
Db 96 YASV-ISSGSEFENAC--GRVDKYLESTLVHSLSIADVAINSLAGTG----- 143

Qy 299 VQRW 302
Db 144 -QRW 146

RESULT 3
T30089

probable zinc proteinase (EC 3.4.24.-) C02G6.1 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30089
R;Bentley, D.; Scheet, P.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid C02G6.
A;Reference number: Z20734
A;Accession: T30089
A;Status: translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-980 <BEN>
A;Cross-references: UNIPROT:Q17592; EMBL:U55372; PIDN:AAA98001.1; GSPPDB:GN00023; CBSP:CG
A;Experimental source: strain Bristol N2; clone C02G6
C;Genetics:
A;Map position: 5
A;Introns: 25/3; 215/2; 266/3; 540/3; 585/3; 786/1; 898/2
C;Keywords: hydrolase; metalloproteinase; zinc
F.73/74/Binding site: zinc (His) #status predicted
F.73/Active site: Glu #status predicted

Query Match 6.3%; Score 104; DB 2; Length 980;
Matches 86; Conservative 67; Mismatches 133; Indels 142; Gaps 22;

Qy 10 HGGASPARVELPTCMYRLPNWNSKTPATAGHVOETTSBPSLQALESDRQDILKRYE 68
Db 276 HKPGPSLIVELKRLGW-VNSIKSDSNITIAAGPGLNLVTDLSTGGLEN-VDEIIQMLNY 333

Qy 69 ---LKAADGLSKWMPDQL-DYT-NLQADEPTLATTN-----LDINSVIGKDY- 116
Db 334 ISMLKSF-GPOQWHDALDSLDSVDFKREKOEQPKMMAINTAASLQYIPIEHLSSYL 391

Qy 117 -----GALKIVINANPASPPLSILVILRLCERYR----- 147
Db 392 LTKYEPERIKLILSTLTPN-----MLVRVUSQRFKEQPGANTIEPVIGTEWMKVTDISPE 445

Qy 148 -----VLSVH- THSSVKNPENLWKCFGEQARKKSRHEYOL----GFTLW---- 189
Db 446 RKKKYENALKTSHHALHLPEKN- EYIATNGQEKPRESVKNEHPKLISDDGWSRWFQKD 503

RESULT 4
B89797
glycerol ester hydrolase [imported] - *Staphylococcus aureus* (strain N315)
C;Species: *Staphylococcus aureus*
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: B89797
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Miutani-Uji, Y.; Kobayashi, N.; Savano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
I;Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant *Staphylococcus aureus*.
A;Reference number: A89758; MURID:21311952; PMID:1148146
A;Accession: B89797
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-691 <KUR>
A;Cross-references: UNIPROT:Q99WQ6; GB:BA000018; PID:g13700235; PIDN:BAB41533.1; GSPPDB:CG
A;Experimental source: strain N315
C;Genetics:
A;Gene: geh
C;Superfamily: *Staphylococcus* triacylglycerol lipase

Query Match 6.0%; Score 99; DB 2; Length 691;
Best Local Similarity 20.2%; Pred. No. 3..4; Mismatches 110; Indels 94; Gaps 15; Matches 65; Conservative 53; Mismatches 110; Indels 94; Gaps 15;

Qy 1 MPMMYQVKPYHGGASPLRVLPELPTOMYRLPNWNSKTPATDA-----GHQVQETSEPSL 52
Db 172 IPAQKVLPKHDKAAPTSTIPS-----NDKTAPKSTKAQDATTDKHPNQDTHOPAH 223

Qy 53 QALERSRQDIDLKLYELLAQAVGLSKM-----HTPDAADL-----VNLQABPTL 101
Db 224 QIIDAKODTV-RQEOKPQVQGDLSKHDGQNSPEKPTDKTDNKLQALQA---PKTR 280

Qy 102 ATNTDLDSVIGKDYGAIKDIVNAPASPPLSILVILRLCERYR-----LNKCPV--VFGFGLGV 161
Db 281 STTNAAD-----AKVRLKANQWP-----LNKCPV-----LNKCPV--VFGFGLGV 318

Qy 162 PENLKCFEG-----EOARKSRHEYOLQGFTLWKNPK-TOMKFSVQTMCPING 209
Db 319 GDNAPALXPNYNGGNKPKVILRKQGYNHQASVSYDRAVELYVIKGGRDVIG 378

Qy 210 EGNIARLPSLEGQKHNAV-----TILTIDSWVIAAMFOLREGSS 249
Db 379 AAHAQKGYHERGKTYKGMNPWEGKKVHLVGHSMGGQTIRLMNBF-----LRNG-N 430

Qy 250 KKAFAVFRSNSALGRSPMIVLWG 271
Db 431 KEBIAHKAHGCEI-SPLPFG 450

RESULT 5
C82441
probable glutathione S-transferase VCA0584 [imported] - *Vibrio cholerae* (strain N16961
C;Species: *Vibrio cholerae*
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

Query Match 100.0%; Score 1655; DB 2; Length 320;
 Best Local Similarity 100.0%; Pred. No. 2.6e-128;
 Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPMYQVQPKPHGGASAPLVELPTCMYRPNHVKTSAPADHVSQETSEPSIQLAESRQ 60
 DR 1 MPMYQVQPKPHGGASAPLVELPTCMYRPNHVKTSAPADHVSQETSEPSIQLAESRQ 60
 DR InterPro: IPR00446; GST_C-term.
 DR IIPRO10987; GST_C-like.
 DR Pfam: PF00043; GST_C; 1.
 DR SEQUENCE 320 AA: 35423 MW: 1C21FLA74C9882B4 CRC64;

QY 61 DILKRLYIKKAADGLSKMHTPDAIDLVTNLQADEPTLTATNTDLSNVLGKGALK 120
 DR 61 DILKRLYIKKAADGLSKMHTPDAIDLVTNLQADEPTLTATNTDLSNVLGKGALK 120
 DR SEQUENCE 320 AA: 35423 MW: 1C21FLA74C9882B4 CRC64;

QY 61 DILKRLYIKKAADGLSKMHTPDAIDLVTNLQADEPTLTATNTDLSNVLGKGALK 120
 DR 61 DILKRLYIKKAADGLSKMHTPDAIDLVTNLQADEPTLTATNTDLSNVLGKGALK 120
 DR SEQUENCE 320 AA: 35423 MW: 1C21FLA74C9882B4 CRC64;

QY 121 DIVINANPASPPLSLVHLRLCERYRVLSTVTHSSVKVNPEVLVKCFCGEQARKQSHE 180
 DR 121 DIVINANPASPPLSLVHLRLCERYRVLSTVTHSSVKVNPEVLVKCFCGEQARKQSHE 180
 DR SEQUENCE 320 AA: 35423 MW: 1C21FLA74C9882B4 CRC64;

QY 181 YOLGFTLIIWKVNPKTQMKFSVQTMCPIEGEGNIAFLSIFGOKHNAVTLLSDWIDIA 240
 DR 181 YOLGFTLIIWKVNPKTQMKFSVQTMCPIEGEGNIAFLSIFGOKHNAVTLLSDWIDIA 240
 DR SEQUENCE 320 AA: 35423 MW: 1C21FLA74C9882B4 CRC64;

QY 241 MFQLREGSSKEAAVFRSMNSALGRSPMWVGNELTVADWLWSLQQTGGSGAAPTNQ 300
 DR 241 MFQLREGSSKEAAVFRSMNSALGRSPMWVGNELTVADWLWSLQQTGGSGAAPTNQ 300
 DR SEQUENCE 320 AA: 35423 MW: 1C21FLA74C9882B4 CRC64;

QY 301 RWLKSCENLAPPSTALQLK 320
 DR 301 RWLKSCENLAPPSTALQLK 320
 DR SEQUENCE 320 AA: 35423 MW: 1C21FLA74C9882B4 CRC64;

RESULT 2

Q8R2Y6 PRIMINARY; PRT; 320 AA.

ID Q8R2Y6 AC 01-JUN-2002 (TREMBREL. 21, Created)
 DT 01-MAR-2004 (TREMBREL. 26, Last annotation update)
 DB Name=Jtvrl;
 GN Mus musculus (Mouse).
 OS Mus musculus (Mouse).
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 SEQUENCE FROM N.A.
 STRAIN=Jtvrl;
 MEDLINE:2238257; PubMed=1477972; DOI=10.1073/pnas.242603899;
 Strausberg R.L., Feinberg E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schueler G.D.,
 Altschul S.F., Zeeberg B., Butet K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 Datchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Usdin T.B., Yoshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Haile S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzy N.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahay J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green D.P., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzywinski M.I., Skalska U., Smialius D.R., Schnurch A., Schein J.E.,
 Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences," Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RL [2]
 RP SEQUENCE FROM N.A.

Q8R2Y6 PRIMINARY; PRT; 320 AA.

ID Q8R2Y6 AC 01-JUN-2002 (TREMBREL. 21, Created)
 DT 01-MAR-2004 (TREMBREL. 26, Last annotation update)
 DB Name=Jtvrl;
 GN Mus musculus (Mouse).
 OS Mus musculus (Mouse).
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 RN [1]
 SEQUENCE FROM N.A.
 TISSUE-Ovary;
 MEDLINE:99056915; PubMed=9878398; DOI=10.1006/jmbi.1998.2316;
 RA Quelillon S., Robinson J.-C., Berthonneau E., Sistecka M., Mirande M.,
 RT "Macromolecular assemblage of aminoacyl-tRNA synthetases: identification of protein-protein interactions and characterization of a core protein," J. Mol. Biol. 285:183-195(1999).
 CC -- FUNCTION: Probable core protein of the multi-synthetase complex which serves as a template for the assembly of the supramolecular structure.
 CC - SUBUNIT: Component of the multi-synthetase complex which is comprised of a bifunctional glutaminyl-prolyl-tRNA synthetase, the non-specific isoleucyl, leucyl, glutamyl, methionyl, lysyl, arginyl, and aspartyl-tRNA synthetases as well as three auxiliary proteins, p18, p48 and p43.
 CC - SIMILARITY: Contains 1 Gtr-like domain.

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CC or send an email to license@ibb-sib.ch)

CC
DR EMBL; AF022727; AAD3422.1; -;
DR InterPro; IPR01987; GST_C-like.
DR InterPro; IPR00046; GST_C-term.

DR Pfam; PF00043; GST_C; 1;
KW protein biosynthesisB

SEQUENCE 320 AA; 35433 MW; 6D24B033ABC810A CRC64;

Query Match 95.0%; Score 1573; DB 1; Length 320;
Best Local Similarity 94.4%; Pred. No. 1.6e-12; Mismatches 12; Indels 0; Gaps 0;

Matches 302; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

RP SEQUENCE OF 197-320 FROM N.A.

RC TISSUE-Fetal liver;

RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Ouyang S., Luo L., Bi J.,

RA Liu M., He F.;

RA "Functional prediction of the coding sequences of 121 new genes deduced by analysis of cDNA clones from human fetal liver.";

RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

RN [4] RT INTERACTION WITH FUBP1.

RX MEDLINE=22716800; PubMed=12819782; DOI=10.1038/ng1182;

RA Kim M.J., Park B.-J., Kang Y.-S., Kim H.J., Park J.-H., Kang J.W., Lee S.W., Han J.M., Lee H.-W., Kim S.;

RT "Downregulation of FUSE-binding protein and c-myc by tRNA synthetase cofactor p38 is required for lung cell differentiation.";

Nat. Genet. 34:330-336 (2003).

-I FUNCTION: Probable core protein of the multisynthetase complex that serves as a template for the assembly of the supramolecular structure. Mediates ubiquitination of FUBP1 and its degradation by the proteasome.

CC CC COFACTOR: Component of the multisynthetase complex which is comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, the monospecific isoleucyl, leucyl, glutamyl, methionyl, lysyl, arginyl, and aspartyl-tRNA synthetases as well as three auxiliary proteins, p88, p88 and p43. Binds FUBP1.

CC CC -I SIMILARITY: Contains 1 GST-like domain.

CC CC -I CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 312.

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CC DR EMBL; U2459; AAC50911.1; ALT FRAME.

DR BC0285; AAH0285.1; -;

DR EMBL; BC010156; AAH10156.1; -;

DR EMBL; AF116615; AAF71039.1; -;

DR H-InvaB; HIX006460; -;

DR MIM; 600859; -;

DR InterPro; IPR01987; GST_C-like.

DR InterPro; IPR00046; GST_C-term.

DR Pfam; PF00043; GSTC; 1.

KW protein biosynthesisB

SEQUENCE 320 AA; 35349 MW; F253726B63C12BAB CRC64;

Query Match 88.5%; Score 1464; DB 1; Length 320;

Best Local Similarity 87.2%; Pred. No. 1.6e-11; Mismatches 279; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

Matches 320; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

RP SEQUENCE OF 197-320 FROM N.A.

RC TISSUE-Lymph;

RA MEDLINE=22788257; PubMed=1247732; DOI=10.1073/pnas.242603899;

RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,

RA Altechul S.P., Zeeberg B.B., Buetow K.H., Schaefer C.C.P., Bhat N.K.,

RA Hopkins R.P., Jordan H., Moore T., Max S. I., Wang J., Haile F.,

RA Diatchenko L., Marusina K., Farmer A.R., Casavant T.L., Schatz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquelandano N.A., Peters G.J., Abramson R.D., Mulahay S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guarratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Murzy D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska M.A., Smilus D.E., Schneich A., Schein J.B., Jones S.J.M., Marra M.A., Snailus D.E., Rodriguez Y.S.N., Krzywinski M.I., Skalska M.A., Smilus D.E., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[3]

RN RN

RP SEQUENCE OF 197-320 FROM N.A.

RC TISSUE-Fetal liver;

RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Ouyang S., Luo L., Bi J.,

RA Liu M., He F.;

RA "Functional prediction of the coding sequences of 121 new genes deduced by analysis of cDNA clones from human fetal liver.";

RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

RN [4]

RT INTERACTION WITH FUBP1.

RX MEDLINE=22716800; PubMed=12819782; DOI=10.1038/ng1182;

RA Kim M.J., Park B.-J., Kang Y.-S., Kim H.J., Park J.-H., Kang J.W., Lee S.W., Han J.M., Lee H.-W., Kim S.;

RT "Downregulation of FUSE-binding protein and c-myc by tRNA synthetase cofactor p38 is required for lung cell differentiation.";

Nat. Genet. 34:330-336 (2003).

-I FUNCTION: Probable core protein of the multisynthetase complex that serves as a template for the assembly of the supramolecular structure. Mediates ubiquitination of FUBP1 and its degradation by the proteasome.

CC CC COFACTOR: Component of the multisynthetase complex which is comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, the monospecific isoleucyl, leucyl, glutamyl, methionyl, lysyl, arginyl, and aspartyl-tRNA synthetases as well as three auxiliary proteins, p88, p88 and p43. Binds FUBP1.

CC CC -I SIMILARITY: Contains 1 GST-like domain.

CC CC -I CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 312.

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CC DR EMBL; U2459; AAC50911.1; ALT FRAME.

DR BC0285; AAH0285.1; -;

DR EMBL; BC010156; AAH10156.1; -;

DR EMBL; AF116615; AAF71039.1; -;

DR H-InvaB; HIX006460; -;

DR MIM; 600859; -;

DR InterPro; IPR01987; GST_C-like.

DR InterPro; IPR00046; GST_C-term.

DR Pfam; PF00043; GSTC; 1.

KW protein biosynthesisB

SEQUENCE 320 AA; 35349 MW; F253726B63C12BAB CRC64;

Query Match 88.5%; Score 1464; DB 1; Length 320;

Best Local Similarity 87.2%; Pred. No. 1.6e-11; Mismatches 279; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

Matches 320; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

RP SEQUENCE OF 197-320 FROM N.A.

RC TISSUE-Lymph;

RA MEDLINE=22788257; PubMed=1247732; DOI=10.1073/pnas.242603899;

RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,

RA Altechul S.P., Zeeberg B.B., Buetow K.H., Schaefer C.C.P., Bhat N.K.,

RA Hopkins R.P., Jordan H., Moore T., Max S. I., Wang J., Haile F.,

RA Diatchenko L., Marusina K., Farmer A.R., Casavant T.L., Schatz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquelandano N.A., Peters G.J., Abramson R.D., Mulahay S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guarratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Murzy D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska M.A., Smilus D.E., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[3]

RN RN

RP SEQUENCE OF 197-320 FROM N.A.

RC TISSUE-Fetal liver;

RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Ouyang S., Luo L., Bi J.,

RA Liu M., He F.;

RA "Functional prediction of the coding sequences of 121 new genes deduced by analysis of cDNA clones from human fetal liver.";

RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

RN [4]

RT INTERACTION WITH FUBP1.

RX MEDLINE=22716800; PubMed=12819782; DOI=10.1038/ng1182;

RA Kim M.J., Park B.-J., Kang Y.-S., Kim H.J., Park J.-H., Kang J.W., Lee S.W., Han J.M., Lee H.-W., Kim S.;

RT "Downregulation of FUSE-binding protein and c-myc by tRNA synthetase cofactor p38 is required for lung cell differentiation.";

Nat. Genet. 34:330-336 (2003).

-I FUNCTION: Probable core protein of the multisynthetase complex that serves as a template for the assembly of the supramolecular structure. Mediates ubiquitination of FUBP1 and its degradation by the proteasome.

CC CC COFACTOR: Component of the multisynthetase complex which is comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, the monospecific isoleucyl, leucyl, glutamyl, methionyl, lysyl, arginyl, and aspartyl-tRNA synthetases as well as three auxiliary proteins, p88, p88 and p43. Binds FUBP1.

CC CC -I SIMILARITY: Contains 1 GST-like domain.

CC CC -I CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 312.

CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.ibb-sib.ch/announce/> or send an email to license@ibb-sib.ch).

CC DR EMBL; U2459; AAC50911.1; ALT FRAME.

DR BC0285; AAH0285.1; -;

DR EMBL; BC010156; AAH10156.1; -;

DR EMBL; AF116615; AAF71039.1; -;

DR H-InvaB; HIX006460; -;

DR MIM; 600859; -;

DR InterPro; IPR01987; GST_C-like.

DR InterPro; IPR00046; GST_C-term.

DR Pfam; PF00043; GSTC; 1.

KW protein biosynthesisB

SEQUENCE 320 AA; 35349 MW; F253726B63C12BAB CRC64;

Query Match 88.5%; Score 1464; DB 1; Length 320;

Best Local Similarity 87.2%; Pred. No. 1.6e-11; Mismatches 279; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

Matches 320; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

RP SEQUENCE OF 197-320 FROM N.A.

RC TISSUE-Lymph;

RA MEDLINE=22788257; PubMed=1247732; DOI=10.1073/pnas.242603899;

RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altechul S.P., Zeeberg B.B., Buetow K.H., Schaefer C.C.P., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S. I., Wang J., Haile F., Diatchenko L., Marusina K., Farmer A.R., Casavant T.L., Schatz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquelandano N.A., Peters G.J., Abramson R.D., Mulahay S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guarratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Murzy D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska M.A., Smilus D.E., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[3]

RN RN

RP SEQUENCE OF 197-320 FROM N.A.

RC TISSUE-Fetal liver;

RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Ouyang S., Luo L., Bi J.,

RA Liu M., He F.;

RA "Functional prediction of the coding sequences of 121 new genes deduced by analysis of cDNA clones from human fetal liver.";

RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

RN [4]

RT INTERACTION WITH FUBP1.

RX MEDLINE=22716800; PubMed=12819782; DOI=10.1038/ng1182;

RA Kim M.J., Park B.-J., Kang Y.-S., Kim H.J., Park J.-H., Kang J.W., Lee S.W., Han J.M., Lee H.-W., Kim S.;

RT "Downregulation of FUSE-binding protein and c-myc by tRNA synthetase cofactor p38 is required for lung cell differentiation.";

Nat. Genet. 34:330-336 (2003).

-I FUNCTION: Probable core protein of the multisynthetase complex that serves as a template for the assembly of the supramolecular structure. Mediates ubiquitination of FUBP1 and its degradation by the proteasome.

CC CC COFACTOR: Component of the multisynthetase complex which is comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, the monospecific isoleucyl, leucyl, glutamyl, methionyl, lysyl, arginyl, and aspartyl-tRNA synthetases as well as three auxiliary proteins, p88, p88 and p43. Binds FUBP1.

CC CC -I SIMILARITY: Contains 1 GST-like domain.

CC CC -I CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 312.

Db 5 QETSEPSLQALESRQDDILKRLYELKAADVGLSKRMHPTDADLVNLQADDEPTTLN 64
 QY 105 TLDNSVUGKDGYGALKDVTINANPASPPLSLVHLRUCERVLTWHSSVKNPEN 164
 Db 65 TUDNSVUGKDGYGALKDVTINANPASPPLSLVHLRUCERVLTWHSSVKNPEN 124
 QY 165 LVKCFGEQARKKOSRHEYOLGFTLJWKVNPKTQMKFSVOTMCPTEGESNIARFLSITGQK 224
 Db 125 LVKCFGEQARKKOSRHEYOLGFTLJWKVNPKTQMKFSVOTMCPTEGESNIARFLSITGQK 184
 QY 225 HNAVLTULSDWIDAMQFOLREGSSKEAVFVFSMSALGREGPWLVNLTVTADWVMSV 284
 Db 185 HNAVLTULSDWIDAMQFOLREGSSKEAVFVFSMSALGREGPWLVNLTVTADWVMSV 244
 QY 285 LOOTGGSSGAAPTNORMIKSCNLAPSTALQLK 320
 Db 245 LOOTGGSSGAAPTNORMIKSCNLAPSTALQLK 280

RESULT 7

O6DKB6 PRELIMINARY; PRT; 311 AA.
 AC O6DKB6:
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DE MCC69221 protein.
 GN Name=MCC69221;
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 OC Xenopidae; Xenopus.
 NCBI_TaxID=8364;
 RP [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Colling F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
 RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquaiello N.A., Peters G.J., Abramson R.D., Mulahay S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blaedel R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
 RA Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences"; RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC074561; AAH74561; -;
 DR InterPro; IPR000464; GST_Cterm.
 DR InterPro; IPR010987; GST_C like.
 DR Pfam; PP00043; GST_C; 1;
 SQ SEQUENCE 311 AA; 34480 MW; D98F27F73C466154 CRC64;

Query Match 69.7%; Score 113.5; DB 2; Length 311;
 Best Local Similarity 67.5%; Pred. No. 6. Be-87%;
 Matches 216; Conservative 49; Mismatches 46; Indels 9; Gaps 3;

RESULT 8

O6INU4 PRELIMINARY; PRT; 311 AA.
 AC O6INU4:
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DE MCC80104 Protein.
 GN Name=MCC80104;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 OC Xenopidae; Xenopus.
 NCBI_TaxID=8355;
 RP [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Ovary;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Colling F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
 RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquaiello N.A., Peters G.J., Abramson R.D., Mulahay S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blaedel R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
 RA Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences"; RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.

RC TISSUE=Ovary;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J.L., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 initiative";
 Dev. Dyn. 225:384-391 (2002).

RN [3]

RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC07178; AAH2178.1; -;
 DR Interpro; IPR004046; GST_Cterm.
 DR Pfam; PF00043; GST_C; 1;
 DR SEQUENCE 311 AA.; 34424 MW; D588325C18D88751 CRC64;

Query Match Best Local Similarity 69.3%; Score 1146.5; DB 2; Length 311; Matches 218; Conservative 44; Mismatches 49; Indels 9; Gaps 3; QY 1 MPMYQVKPVHGGSAPRLVPLPTCMRLPNTVHSKITSPTADAGHVOETSEPSIQALESRD 60 Db 1 MPMYQVKPVHGGSAPRLVPLPTCMRLPNTVHSKITSPTADAGHVOETSEPSIQALESRD 52

QY 61 DILKRYELKAADVGLSKMHTPDADLVNLOADEPTLTATNLIDNSVLGDKYGAALK 120 Db 53 DILKRYELKAADVGLSKMHTPDADLVNLOADEPTLTATNLIDNSVLGDKYGAALK 112

QY 121 DIVINANPASPLSLVILRLLCERYQVLSAVHTHSSTISIPEPLIKCFGDKMKRHE 180 Db 113 DIVINANPASPLSLVILRLLCERYQVLSAVHTHSSTISIPEPLIKCFGDKMKRHE 172

QY 181 YOLGFTLWVNPKVQPKOMKSVQTMCPIEGHGNARFLSIFGOKHNAVTTLIDSWDIA 240 Db 173 YOLGFTLWVNPKVQPKOMKSVQTMCPIEGHGNARFLSIFGOKHNAVTTLIDSWDIA 232

QY 241 MFOLREGSSKEKAVALKANTALGKSPWLGVNLTVADIVSWCAVOCGNST-AVPVNQ 300 Db 233 MFOLREGSSKEKAVALKANTALGKSPWLGVNLTVADIVSWCAVOCGNST-AVPVNQ 291

QY 301 RWLKCSCENLAPFSTALQIK 320 Db 292 KWWKSCENLAPFSTALQIK 311

Db 292 KWWKSCENLAPFSTALQIK 311

RESULT 9

Q7ZYD7 PRELIMINARY; PRT; 311 AA.
 ID Q7ZYD7
 AC
 DT 01-JUN-2003 (TREMBREL. 24, Created)
 DT 01-JUN-2003 (TREMBREL. 24, Last sequence update)
 DE JEV1-prov protein.

OS Xenopus laevis (African clawed frog).
 OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Xenopidae; Xenopus.
 OC Xenopidae; Xenopus.
 OK NCBI_TaxID=8355;
 RN [1]

SEQUENCE FROM N.A.
 RP
 RC
 MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Caravant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Trohiuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,
 RA Bosak S.A., McWain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Farley J., Helton E., Keestman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Shervchenko Y., Boutefeld G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.C., Stalska U., Smilus D.E., Schnurch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA [1]

RESULT 10

Q7T3C0 PRELIMINARY; PRT; 321 AA.
 ID Q7T3C0
 AC
 DT 01-OCT-2003 (TREMBREL. 25, Created)
 DT 01-OCT-2003 (TREMBREL. 25, Last sequence update)
 DE ZGB:63976.
 GN ORFNAMES-ZGB:63976;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC
 OC
 OC
 OC
 OC
 OC
 RN [1]

SEQUENCE FROM N.A.
 RP
 RC
 TISSUE=Kidney;
 RA MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heileh F.,
 RA Diatchenko L., Maruyama K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Schetetz T.E.,
 RA Brownstein M.J., Usdin T.B., Tsoiuruki S., Carrinci P., Prange C.,
 RA Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mulahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Soergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettlerman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinwood J., Smailus D.E., Scherch A., Schein J.B.,
 RA Krzywinski M.I., Skalska U., Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15, 000 full-length human
 RT and mouse cDNA sequences,"
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Submittd (JUN 2003) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; BC03178; AAH31781; -; zc:63976.
 DR ZFIN; ZDB-GENE:040426-2652; zc:63976.
 DR InterPro; IPR010987; GST_C-like.
 DR Pf00044; GST_C; 1;
 SQ SEQUENCE 321 AA; 34852 MW; BA0F6B951208244A CRC64;
 Query Match 56.0%; Score 926.5; DB 2; Length 321;
 Best Local Similarity 57.3%; Pred. No. 4.1e-68;
 Matches 188; Conservative 48; Mismatches 77; Indels 15; Gaps 7;
 QY 1 NPMVQKPHGGSAPRURVELPOMXKULPNVHSKTS--PATDAGHQVETSSEPSLOAES
 Db 1 NPMVQKPHGGSAPRURVELPOMXKULPNVHSKTS--PATDAGHQVETSSEPSLOAES 57
 QY 58 RQDDILKRLYELKAAVDGSKMHTPADDVTNI---QADDEPTLATNTLDNSVLGK 114
 Db 55 RQDEILKRLYELKAATVDGLAKVTTDADLRASTLAHTLTHTPADAVLRGTAIDLIGK 114
 QY 115 RQGALKDIVINANPAPPLSLVHLRUCBRYRVISTVHTTSSVKVNPEVNLKCFG-EQA 173
 Db 115 DIGALRDLIVINANPAPPLSLVHLRUCBRYRVISTVHTTSSVKVNPEVNLKCFG-EQA 173
 QY 174 RKQSREHYOLQFTLIMKVNPKTMQKSQVMTCPIEBGRNIRFLSFLG-QKHNAYLT 232
 Db 175 HSYARFRQFGTLTQDVSQKLKSTONQCPIDEGVRVFLYPLGPRPVATL 234
 QY 233 IDSWVDIAMFOLREGSSKEKAVFRSMNSALGRSPWLVNGNEITVAUWVMSVLQTGGSS 292
 Db 235 MDGWDTALRQLAEQGSKERAAVRNALANGRSPWLVQGSPSLADIVSACCVLQQTGS 294
 QY 293 GAAPTNVORMWIKSCENLAPFSTALQIK 320
 Db 295 -SAPANVQRWIKSCONLGYFSCVDPLQ 321
 RESULT 11
 ID Q7Q7A3 PRELIMINARY; PRT; 340 AA.
 AC Q7Q7A3; PRELIMINARY;
 DT 01-MAR-2004 (T=EMBLrel. 26, Created)
 DT 01-MAR-2004 (T=EMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (T=EMBLrel. 26, Last annotation update)
 DE AGCP808 (fragment)
 GN Name=agCG0514; ORFnames=ENSAG00000011827;
 OS Anopheles gambiae ST. PEST.
 OC Baktarya; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriidae; Drosophilidae; Drosophila.
 NCBI_TAXID=7227;
 RN SEQUENCE FROM N.A.
 RP MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Richards J., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfleiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Holt G., Nelson C.R., Gabor G.L.,
 RA Abrial J.F., Asburyani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Balow R.M., Basu P., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brodtier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabelli A.B., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA SEQUENCE FROM N.A.
 RP

QY 168 CFGEQARKQSRRHEYQLOFTLWKVNPVKTQMFESVQTMCPICEGEGNARFLPSLFGOKHNA 227 DT 16-OCT-2001 (Rel. 4.0, Last sequence update)
 Db 171 VEVNPALP-----KSVTLLWNCNTTEMSSPTMWPYPIGEVNTRYRGRGVPAEYR 224 DT 25-JAN-2005 (Rel. 4.6, Last annotation update)
 AC Q6NK04; 06NK04; 06NK04; PRELIMINARY; PRT; 322 AA. DE probable multisynthetase complex auxiliary component p18.
 ORFNames=CG12394;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriidae; Drosophilidae; Drosophila;
 OC NCBI_TaxID=7227;
 Db 285 L 285 RN [1]
 Db 285 L 285 RN
 RP STRAIN=Berkeley;
 RX SEQUENCE FROM N.A.
 RA MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Cainiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanaiades P.G., Scherer S.E., Li P.W., Hoskins R.A., Gallo R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agayamani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Balow R.M., Beau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brodatine P., Brotter P.,
 RA Burtis K.C., Buchan M.A., Butler H., Cadile A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin R.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris P.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston T.J., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Kotchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei Y., McIntosh J., McLeod M.P., McPherson D.,
 RA Merkulov G., Milashina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muny D.M., Neilson D.L.,
 RA Hostin D., Houston T.J., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Nelson D.R., Neilson K.A., Nixon K., Nuneskern D.R., Pacieb J.M.,
 RA Palazzolo M., Pitman G.S., Pan S., Pollard J., Purif V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupsik M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.-A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.-H., Zhong F., Zhong W., Zhou X., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster.",
 RT Science 287:2185-2195 (2000).
 RN [2]
 RP GENOME REANNOTATION.
 RX MEDLINE=22426059; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berlin B.P.,
 RA Bettencourt B.R., Cainiker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.",
 RT Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
 RL "Annotation of the Drosophila melanogaster euchromatic genome: a
 RL systematic review.",
 CC - FUNCTION: Probable core protein of the multisynthetase complex
 CC that serves as a template for the assembly of the supramolecular
 CC structure (By similarity).
 CC - SUBUNIT: Component of the multisynthetase complex which is
 CC comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, the
 monospecific isoleucyl-, leucyl-, glutaminyl-, methionyl-, lysyl-,
 arginyl-, and aspartyl-tRNA synthetases as well as three auxiliary
 CC proteins, p18, p48 and p43 (By similarity).
 CC - SIMILARITY: Contains 1 Gsr-like domain.

RESULT 15
 MCA2_DROME STANDARD; PRT; 334 AA.
 ID 09VUR3; 16-OCT-2001 (Rel. 4.0, Created)

CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>)
 or send an email to license@isb-sib.ch).

CC

DR EMBL; AB003530; AAAF49612.1; -.

DR FLYBase; FBgn0036515; CG32304.

DR InterPro; IPR010987; GST_C-like.

DR InterPro; IPR004046; GST_C-term.

DR PFam; PF00043; GST_C; 1.

KW protein biosynthesis.

FT DOMAIN 280 327

SQ SEQUENCE 334 AA; 36933 MW; B68FD70AE621990F CRC64;

Query	Match	Similarity	Score	DB	Length	Matches	Pred.	No.	2e-09;	Mismatches	124;	Indels	73;	Gaps	9;	
Qy	3 MYQVKPYHGGSSAPLRLPEVLPCTMYRILPVN-----HSKNTSPATDAG-----	13.1%	216.5	DB 1	334											42
Db	1 MYELKTL--LPQFDIKLPIPMYRILPVN-----HSKNTSPATDAG-----															57
Qy	43 -----RVOETSEPSIQLAESRQDDLIKRUYELKAADVGIISKMIHTPD															84
Db	58 RTGIRNAATCGLDLSLGROIQRLKDDTASVAARQEKKLQFELKQHQQR-----															110
Qy	85 ADDPVTNLILQADEPPTLATNTLDLNLSVLGKGDKYALKDVINANPASPLSLIVHLRICE															144
Db	111 AGLGVCG--RTFOHTTAFONG-----GKVEVPLQDVINGHNPFFIPYALLALKAWN															161
Qy	145 RYRVLSTVTHHSSKVN-----PENIVCFEQARKQSSRHYQOLGFTLWKVNKTQM															197
Db	162 LYTTIDVKTPFHSTMADIGPAREFEANLAKVPUVNPALP-----KISVTLWKNCHEITEM															215
Qy	198 KFSVQITMCPIEGEONIARFLPSIFGOKENAVTML---IDSWMIDAMFQLEBGSSEKAA															254
Db	216 ISSPTMVYPIYGWNILRYLGRVGPAPVTRYEGSSPLCMEIDLVIDICQQLRCNTHKQVA															275
Qy	255 VFRSMNSALGRSPWLGVGNELTVADVWVSL															285
Db	276 MVRLLDQKLUQKOOYFGGSQMSVADNGVSSL															306

Search completed: February 23, 2005, 13:57:14
 Job time : 62.9811 secs

GenCore version 5.1.6
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Om protein - protein search, using sw model

Run on: February 23, 2005, 13:25:39 ; Search time 70.371 seconds

1758.725 Million cell updates/sec

Title: US-10-622-817-6

Perfect score: 1655

Sequence: 1 MPMYQVKPYHGGSAPLRVEL.....RWLRKSCENLAPFSTALQQLK 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqb, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseq1990:*

2: geneseq1990s:*

3: geneseq2000s:*

4: geneseq2001:*

5: geneseq2002s:*

6: geneseq2003as:*

7: geneseq2003bs:*

8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1464	88.5	320	AAB58613
2	1464	88.5	320	AABW0843
3	1436	86.8	312	AJW25776
4	1435	86.8	312	ADRB6551
5	1232	74.4	272	ADC10204
6	1069	64.6	229	ADRB86553
7	735	44.4	161	ADRB86552
8	248	15.0	51	ABP01502
9	216.5	13.1	334	ABG22468
10	148	8.9	263	ABG23964
11	126.5	7.6	716	AGC41411
12	126.5	7.6	719	AGC41410
13	126.5	7.6	748	AGC41409
14	106	6.4	1512	AGU04349
15	106	6.4	1512	AKM78732
16	106	6.4	1550	AMN79716
17	104	6.3	980	ADM23683
18	102	6.2	1049	ADM67090
19	101.5	6.1	724	AGB85046
20	99	6.0	691	ABU16445
21	98	5.9	243	ABU51858
22	98	5.9	243	ABM54577
23	98	5.9	6	ABJ18952
24	98	5.9	694	Aau34345
25	98	5.9	690	ABW71749

ALIGNMENTS

26	98	5.9	985	8	ADN88622	Adn88622 Rat epid
27	98	5.9	997	8	ADN88620	Adn88620 Rat epid
28	98	5.9	1004	8	ADN88621	Adn88621 Rat epid
29	98	5.9	1013	8	ADN88594	Adn88594 Rat epid
30	98	5.9	1016	8	ADN88619	Adn88619 Rat epid
31	98	5.9	1032	8	ADN88618	Adn88618 Rat epid
32	96.5	5.8	1398	8	ABM83058	Abm83058 Human dia
33	96.5	5.8	1398	8	ABM83057	Abm83057 Human dia
34	96.5	5.8	1440	8	ADN03674	Adn03674 Antipsoni
35	96.5	5.8	1440	8	ADP54124	Adp54124 Human PRO
36	96.5	5.8	1440	8	ADP23041	Adp23041 PRO polyp
37	96	5.8	2273	2	AAB98811	Aar98811 Eryspile
38	95	5.7	722	8	ABD20980	Abd20980 Bacterial
39	94	5.7	436	5	ABP54068	Abp54068 Lactococc
40	93.5	5.6	1049	5	ABR91239	Abbr91239 Heribocida
41	93.5	5.6	1064	5	ABE25162	Aee25162 RCH1.5 pr
42	93.5	5.6	1090	4	ABC17694	Abg17694 Novel hum
43	93.5	5.6	1090	4	ABG18331	Abg18331 Novel hum
44	93	5.6	204	8	ADS21772	Abd21772 Bacterial
45	93	5.6	559	2	AAR10682	Har10682 Polyhydro

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1464	88.5	320	kde5813 Human Pro
2	1464	88.5	320	Abm80843 Tumour-ab
3	1436	86.8	312	Raw25776 JTV1 prot
4	1435	86.8	312	ADRB6551 1-312 ami
5	1232	74.4	272	ADC10204 Human Nov
6	1069	64.6	229	ADRB86553 84-312 ami
7	735	44.4	161	ADRB86552 1-161 ami
8	248	15.0	51	ABP01502 Human ORF
9	216.5	13.1	334	ABB62468 Drosophil
10	148	8.9	263	ABG23964 Novl hum
11	126.5	7.6	716	AGC41411 Arabidps
12	126.5	7.6	719	AGC41410 Arabidps
13	126.5	7.6	748	AGC41409 Arabidps
14	106	6.4	1512	Aau04349 Mammalian
15	106	6.4	1512	Ham78732 Human pro
16	106	6.4	1550	Ham79716 Human pro
17	104	6.3	980	Adn23683 Bacterial
18	102	6.2	1049	Abm67090 Photorhab
19	101.5	6.1	724	Agb85046 Shrimp wh
20	99	6.0	691	Abu16445 Protein e
21	98	5.9	243	Aau58158 Propionib
22	98	5.9	243	Abm54577 Propionib
23	98	5.9	6	Abj18952 Pathogen
24	98	5.9	694	Aau34345 Staphyloc
25	98	5.9	690	Abw71749 Staphyloc

subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at <http://wipo.int/pct/published/pct.html>.

29-SEP-2003; 2003WO-US028547.
02-OCT-2002; 2002US-0414971P.
(GETH) GENENTECH INC.
Wu TD, Zhang Z, Zhou Y;
WPI; 2004-347921/32.
N-PSDB; ACN38579.

New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or prostate cancer or tumor.

Claim 12: SEQ ID NO: 2179: 7273m. English

XX SQ Sequence 320 AA;

The invention relates to human tumour-associated antigenic target (TAT) polypeptides, nucleic acids encoding them, and methods for their use.

Query Match	Score 1464;	DB 7;	Length 320;
Best Local Similarity	87.2%	Pred. No.	7.5e-142;
Matches	279;	Conservative	16;
Mismatches	27;	Indels	0;
Gaps	0		
Qy			
1	MPMKVKVPHGGSAPLRVEPTCMWLRPNHRSKTPATDGHVQBTSEPSLQALERSQD	60	
Db	1 MPMQVKVPHGGSAPLRVEPTCMWLRPNHRSKTPATDGHVQBTSEPSLQALERSQD	60	
Qy			
61	DILKRLYELKAVADGLSKMQTDPADLVDVNTIQADEPTLTINADLNSVLKGROYALK	120	
Db	61 DILKRLYELKAVADGLSKMQTDPADLVDVNTIQADEPTLTINADLNSVLKGROYALK	120	
Qy			
121	DIVINANPAPPLSLVHLRLLCERYVRLSTVHTHSVKVNPEVJYCFEQARKQSRRHE	180	
Db	121 DIVINANPAPPLSLVHLRLLCERYVRLSTVHTHSVKVNPEVJYCFEQARKQSRRHE	180	
Qy			
181	YOLGFTLIWKVNPQTKOMKSQVQTMPIEGEYGNIAFLPSLFGQRNNAVITLISWNDIA	240	
Db	181 YOLGFTLIWKVNPQTKOMKSQVQTMPIEGEYGNIAFLPSLFGQRNNAVITLISWNDIA	240	
Qy			
241	MFQLEREGSSREKAAVPRSHMSALGSRSPWLGVNELTIVADYLWSVHQQTGGSSGAAPTNO	300	
Db	241 IFQLEKGSSREKAAVPRSHMSALGSRSPWLGVNELTIVADYLWSVHQQTGGSSGAAPTNO	300	
Qy			
301	RWLUKSCENLAPESTALQLIK	320	
Db	301 RWMRSCENLAPENTALKLIK	320	
RESULT 2			
ABM8043			
ID	ABM8043 standard; protein; 320 AA..		
XX			
AC	ABM8043;		
XX			
DT	18-NOV-2004 (first entry)		
XX			
DE	Tumour-associated antigenic target (TAT) polypeptide PROB1501, SEQ:2179.		
XX			
KW	Tumour-associated antigenic target; TAT; human; overexpression; cancer; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; Leukemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytostatic.		
XX			
OS	Homo sapiens.		
XX			
PN	WO2004030615-A2.		
XX			
PD	15-APR-2004.		

polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids and antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome mapping, in gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT polypeptide of the invention.

ID AAW25776 Standard; protein; 312 AA.
 XX
 AC AAW25776;
 XX
 DT 19-DBC-1997 (first entry)
 XX
 DB JTV1 protein.
 XX
 KW JTV1; hPMS2; probe; detection; chromosome 7; deletion; mismatch repair gene; hereditary non-polyposis colorectal cancer; homologous recombination.
 XX
 OS Homo sapiens.
 XX
 PN WO9708312-A1.
 XX
 PD 06-MAR-1997.
 XX
 PP 26-AUG-1996; 96WO-US013598.
 XX
 PR 24-AUG-1995; 95US-00518862.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Vogelstein B, Kinzler KW, Nicolaides NC;
 XX
 PT Novel chromosome 7 gene, JTV1 - used for detecting chromosome 7 deletions, and PMS2 promoter activity.
 XX
 PS Claim 5; Fig 2; 31pp; English.
 XX
 CC This sequence is JTV1 protein and is encoded by DNA isolated from human chromosome 7. The JTV1 coding sequence is located upstream from hPMS2. JTV1 cDNA can be used as probes to detect chromosome 7 deletions involving JTV1. Due to the overlapping promoter regions, deletions of JTV1 would also affect PMS2 (a mismatch repair gene) expression, leading to hereditary non-polyposis colorectal cancer. JTV1 can also be used to assay activity or competence of the PMS2 promoter region, the presence of JTV1 suggesting that the PMS2 promoter is intact. JTV1 sequences can also be used to guide homologous recombination at the PMS2 locus
 CC Sequence 312 AA:
 Query Match 86.8%; Score 1436; DB 2; Length 312;
 Best Local Similarity 87.5%; Pred. No. 5.6e-139; Mismatches 273; Conservative 14; Indels 0; Gaps 0;
 Matches 121; Sequence 312 AA:
 CC 1 NPMYQVTPKPGGASAPLRLVTPCMYLPNVSKTSPATDGHVOTSEPSLSQALERSQD 60
 CC 1 NPMYQVTPKPHGGAPPLRVELPTCMYLPNVHGRSGYPAGPGHVOESNLSQLAERSQD 60
 Db 61 DILKRLYELKAADVGLSKMHTPDAVLVNTILOADEPTTLTNALDNLNSLGKOGALK 120
 Db 61 DILKRLYELKAADVGLSKMHTPDAVLVNTILOADEPTTLTNALDNLNSLGKOGALK 120
 Qy 121 DIVINANPASPPLSLVHLRLCERYRLVSTVHTISSVKNPENLVCFGEQARKRSRHE 180
 Db 121 DIVINANPASPPLSLVHLRLCERYRLVSTVHTISSVKNPENLVCFGEQARKRSRHE 180
 Qy 181 YOLGFPLIWKVPKTOMKFSYOTMCIEGENIARFLSLGOKENAVLTLLIDSWDIA 240
 Db 181 YOLGFPLIWKVPKTOMKFSYOTMCIEGENIARFLSLGOKENAVLTLLIDSWDIA 240
 Qy 241 MQLREGSSKSKKAAVRSMNSALGRPMIVNELTADWVWVSIQQTGESSGAQPTNVO 300
 Db 241 MQLREGSSKSKKAAVRSMNSALGRPMIVNELTADWVWVSIQQTGESSGAQPTNVO 300
 Qy 301 RWLKSCENLAPP 312
 Db 301 RWLKSCENLAPP 312

RESULT 4
 ID ADR86551
 ID ADR86551 Standard; protein; 312 AA.
 XX
 AC ADR86551;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE 1-312 amino acid sequence of p38/JTV-1 protein.
 XX
 KW p38/JTV-1; Cytostatic; cancer; leukemia; anticancer.
 XX
 OS Homo sapiens.
 XX
 PN EP1454628-A2.
 XX
 PD 08-SEP-2004.
 XX
 PR 09-SEP-2003; 2003EP-00020344.
 XX
 BR 03-MAR-2003; 2003KR-00013058.
 XX
 PA (UYSE-) UNIV SEOUL NAT IND FOUND.
 XX
 DR WPI; 2004-627822/61.
 XX
 DR N-PSDB; ADR86548.
 XX
 PR Kim S, Park B;
 XX
 PT New isolated p38/JTV-1 protein, useful as medicament for treating cancer e.g., stomach, liver, blood, bone, pancreatic, skin, head or neck cancer and cutaneous or intraocular melanoma, as well as for screening new anticancer agents.
 XX
 PR Claim 5; SEQ ID NO 4; 47pp; English.
 XX
 The present invention relates to an isolated p38/JTV-1 protein for use as medicament. The p38/JTV-1 protein or the pharmaceutical composition is useful as medicament for treating breast cancer, large intestinal cancer, lung cancer, small cell lung cancer, stomach cancer, head or neck cancer, blood cancer, bone cancer, pancreatic cancer, skin cancer, head or neck cancer, rectal cancer, colon cancer, cervical cancer, vulval cancer, vaginal carcinoma, endometrial carcinoma, cervical cancer, small intestine cancer, endocrine Hodgkin's disease, esophageal cancer, adrenal cancer, soft tissue cancer, thyroid cancer, parathyroid cancer, adrenal cancer, chronic or acute tumour, urethral cancer, penile cancer, prostate cancer, chronic or acute leukaemia, lymphocytic lymphoma, bladder cancer, kidney cancer, ureter cancer, renal cell carcinoma, renal pelvic carcinoma, CNS tumour, primary CNS lymphoma, bone marrow tumour, brain stem nerve gliomas, pituitary adenoma, or their combination. The protein is useful as a target for screening new anticancer agents. The present sequence represents the 1-312 amino acid sequence of p38/JTV-1 protein.
 CC Sequence 312 AA:
 Query Match 86.8%; Score 1436; DB 8; Length 312;
 Best Local Similarity 87.5%; Pred. No. 5.6e-139; Mismatches 273; Conservative 14; Indels 0; Gaps 0;
 Matches 121; Sequence 312 AA:
 CC 1 NPMYQVTPKPGGASAPLRLVTPCMYLPNVSKTSPATDGHVOTSEPSLSQALERSQD 60
 CC 1 NPMYQVTPKPHGGAPPLRVELPTCMYLPNVHGRSGYPAGPGHVOESNLSQLAERSQD 60
 Db 61 DILKRLYELKAADVGLSKMHTPDAVLVNTILOADEPTTLTNALDNLNSLGKOGALK 120
 Db 61 DILKRLYELKAADVGLSKMHTPDAVLVNTILOADEPTTLTNALDNLNSLGKOGALK 120
 Qy 121 DIVINANPASPPLSLVHLRLCERYRLVSTVHTISSVKNPENLVCFGEQARKRSRHE 180
 Db 121 DIVINANPASPPLSLVHLRLCERYRLVSTVHTISSVKNPENLVCFGEQARKRSRHE 180
 Qy 181 YOLGFPLIWKVPKTOMKFSYOTMCIEGENIARFLSLGOKENAVLTLLIDSWDIA 240
 Db 181 YOLGFPLIWKVPKTOMKFSYOTMCIEGENIARFLSLGOKENAVLTLLIDSWDIA 240
 Qy 241 MQLREGSSKSKKAAVRSMNSALGRPMIVNELTADWVWVSIQQTGESSGAQPTNVO 300
 Db 241 MQLREGSSKSKKAAVRSMNSALGRPMIVNELTADWVWVSIQQTGESSGAQPTNVO 300
 Qy 301 RWLKSCENLAPP 312
 Db 301 RWLKSCENLAPP 312

QY 181 YOLGFTLWKNVPTKTONKFPSVQTMCPIEGEGNIAFLPLFSLPGQKHNAVTLLIDSWDIA 240
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 PR XX PA (CURA-) CURAGEN CORP.
 PR 181 YOLGFTLWKNVPTKTONKFPSVQTMCPIEGEGNIAFLPLFSLPGQKHNAVTLLIDSWDIA 240
 PR XX PA
 PR QY 241 MFLRGSSKKEKAVERSMRMSALGSPWMVNLTVADVVLWSLQQTGGSSGAPINQ 300
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 PR XX PA
 PR Db 241 IFLQKEGSSKKEKAVERSMRMSALGSPWMVNLTVADVVLWSLQQTGGSSGAPINQ 300
 PR XX PA
 PR QY 301 RWLKSCENTLAPP 312
 :|||||:
 PR XX PA
 PR Db 301 RWMRSCENTLAPP 312
 PR XX PA
 PR RESULT 5
 PR ADC10204
 PR ID ADC10204 standard; protein; 272 AA.
 PR AC XX
 PR AC ADC10204;
 PR DT XX
 PR 18 - DBC-2003 (First entry)
 PR DE Human NOVX polypeptide SEQ ID NO: 226.
 PR XX
 PR KW cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective;
 PR KW antiinflammatory; gene therapy; anticancer therapy; thyromimetic; NOVX;
 PR KW pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;
 PR KW inflammatory disorder; chromosome mapping; tissue typing;
 PR KW predictive medicine.
 PR XX
 PR OS Homo sapiens.
 PR XX
 PR PN WO2003000842-A2.
 PR XX
 PR PD 03-JAN-2003.
 PR XX
 PR PF 04-JUN-2002; 2003WO-US017443.
 PR XX
 PR 04-JUN-2001; 2001US-0295607P.
 PR PR 04-JUN-2001; 2001US-029561P.
 PR PR 06-JUN-2001; 2001US-0296494P.
 PR PR 06-JUN-2001; 2001US-0296418P.
 PR PR 07-JUN-2001; 2001US-0296575P.
 PR PR 11-JUN-2001; 2001US-029714P.
 PR PR 12-JUN-2001; 2001US-0295573P.
 PR PR 12-JUN-2001; 2001US-0297567P.
 PR PR 14-JUN-2001; 2001US-0298285P.
 PR PR 15-JUN-2001; 2001US-0298288P.
 PR PR 18-JUN-2001; 2001US-0299133P.
 PR PR 19-JUN-2001; 2001US-0299230P.
 PR PR 21-JUN-2001; 2001US-029949P.
 PR PR 22-JUN-2001; 2001US-0300177P.
 PR PR 26-JUN-2001; 2001US-0300883P.
 PR PR 28-JUN-2001; 2001US-0301530P.
 PR PR 28-JUN-2001; 2001US-0301550P.
 PR PR 03-JUL-2001; 2001US-030291P.
 PR PR 31-JUL-2001; 2001US-0308890P.
 PR PR 14-SEP-2001; 2001US-034669P.
 PR PR 25-SEP-2001; 2001US-034669P.
 PR PR 03-DEC-2001; 2001US-0337477P.
 PR PR 14-DEC-2001; 2001US-0341562P.
 PR PR 21-FEB-2002; 2002US-0388656P.
 PR PR 22-FEB-2002; 2002US-0359122P.
 PR PR 22-FEB-2002; 2002US-0358978P.
 PR PR 22-FEB-2002; 2002US-0359034P.
 PR PR 22-FEB-2002; 2002US-0359035P.
 PR PR 27-FEB-2002; 2002US-0359121P.
 PR PR 01-MAR-2002; 2002US-0360858P.
 PR PR 12-MAR-2002; 2002US-0363430P.
 PR PR 12-MAR-2002; 2002US-0363676P.
 PR PR 10-APR-2002; 2002US-0371346P.
 PR PR 10-MAY-2002; 2002US-037944P.

PR 04-JUN-2002; 2002US-0037944. PR XX
 PR (CURA-) CURAGEN CORP. PR XX
 PR Agree MS., Anderson DW, Berghs C, Casman SJ, Catterton E;
 PR PI Dipiippo VA, Edinger SR, Eisen A, Ellerman K, Gangoli BA;
 PR PI Gerlach VL, German L, Guo X, Heermann JL, Hjalt T, Ji W, Kekuda R;
 PR PI Khramtsov NV, Li L, Liu X, Malvankar UM, Miller CB, Millet I;
 PR PI Ort T, Padigaru M, Patterson M, Pena CEA, Rastelli L, Rieger DK;
 PR PI Rothenberg ME, Sherry SG, Shimkets RA, Smitson G, Spoderna SK;
 PR PI Spytek KA, Stone DR, Vernet CAM, Zhong H, Zhou M, Alsobrook JP;
 PR PI Burgess CE, Lepley DM;
 PR XX DR Burges CE, Lepley DM;
 PR XX DR N-PSDB; ADC10203.
 PR XX PT New isolated NOVX polypeptides and nucleic acid molecules useful for
 PR PT treating, preventing, and diagnosing pathological conditions with NOVX-
 PR PT associated disorders, such as cancer, obesity, diabetes and inflammatory
 PR XX or CNS diseases. PR XX
 PR PS Claim 1; SEQ ID NO 226; 772pp; English.
 PR XX
 PR CC The invention relates to novel isolated polypeptides, mature form of the
 PR CC polypeptide, a sequence that is 95% identical to the polypeptide or the
 PR CC polypeptide comprising one or more conservative substitutions. The NOVX-
 PR CC polypeptide is useful for treating or preventing a pathology associated
 PR CC with the polypeptide e.g. disorders associated with aberrant expression
 PR CC or activity of the polypeptide, such as cancer, diabetes, obesity, and
 PR CC endocrine, CNS and inflammatory disorders. They can also be used in
 PR CC various detection and screening assays, chromosome mapping, tissue typing
 PR CC and predictive medicine. This sequence corresponds to one of the
 PR XX polypeptides of the invention.
 PR Sequence 272 AA;

PR Query Match 74.4%; Score 1232; DB 7; Length 272;
 PR Best Local Similarity 88.4%; Pred. No. 5. 1e-118; Mismatches 19; Indels 0; Gaps 0;
 PR Matches 237; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

PR QY 45 QESBPSIQALESRQDDILKRLKYLEKAZAVDGSLSKMHTPDADLYNTLOADEPTLTN 104
 PR DB 5 QBSNLSQALRSRQQDILKRLKYLEKAZAVDGSLSKMHTPDADLYNTLOADEPTLTN 64
 PR QY 105 TIDLNSVKGDKDYGALKDVIVNANPASPPSLSLVHLRLLCERYRVSTVHHSVYKPN 164
 PR DB 65 ALDILNSVKGDKDYGALKDVIVNANPASPPSLSLVHLRLLCERYRVSTVHHSVYKPN 124
 PR QY 165 LYKCFGSGQARKSRSRQHRYQGLGTLLWKNVPTKTONKFPSVQTMCPIEGEGNIAFLPLFSLPGOK 224
 PR DB 125 LYKCFGSGQARKSRSRQHRYQGLGTLLWKNVPTKTONKFPSVQTMCPIEGEGNIAFLPLFSLPGOK 184
 PR QY 225 HNAVTLLIDSWDIDAMFQREGSSKKEKAVERSMRMSALGSPWMVNLTVADVVLWSV 284
 PR DB 185 HNAVTLLIDSWDIDAMFQREGSSKKEKAVERSMRMSALGSPWMVNLTVADVVLWSV 244
 PR QY 285 LQQTGGSSGAAPTNVORWLMKSCENLAPP 312
 PR DB 245 LQQTGGSSGAAPTNVORWLMKSCENLAPP 272

PR RESULT 6
 PR ADR86553 standard; protein; 229 AA.
 PR ID ADR86553
 PR XX AC ADR86553;
 PR XX DT 18-NOV-2004 (first entry)
 PR XX DE 84-12 amino acid sequence of p38/JTV-1 protein.
 PR XX KW p38/JTV-1; Cytostatic; cancer; leukemia; anticancer.
 PR XX

OS Homo sapiens.
 XX
 PN EP1454628-A2.
 XX
 PD 08-SEP-2004.
 XX
 PR 09-SEP-2003; 2003EP-00020344.
 XX
 PR 03-MAR-2003; 2003KR-00013058.
 XX
 PA (UYSE-) UNIV SEOUL NAT IND FOUND.
 XX
 PI Kim S., Park B;
 XX
 DR WPI; 2004-627822/61.
 DR N-PSDB; ADR86550.
 XX
 PT New isolated p38/JTV-1 protein, useful as medicament for treating cancer e.g., stomach, liver, blood, bone, pancreatic, skin, head or neck cancer and cutaneous or intracocular melanoma, as well as for screening new anticancer agents.

XX
 Claim 5; SEQ ID NO 6; 47pp; English.

The present invention relates to an isolated p38/JTV-1 protein for use as medicament. The p38/JTV-1 protein or the pharmaceutical composition is useful as medicament for treating breast cancer, large intestinal cancer, lung cancer, small cell lung cancer, stomach cancer, liver cancer, blood cancer, bone cancer, pancreatic cancer, skin cancer, head or neck cancer, cutaneous or intracocular melanoma, uterine carcinoma, ovarian cancer, rectal cancer, anal cancer, colon cancer, fallopian tube carcinoma, endometrial carcinoma, cervical cancer, vulval cancer, vaginal carcinoma, Hodgkin's disease, esophageal cancer, small intestine cancer, endocrine cancer, thyroid cancer, parathyroid cancer, adrenal cancer, soft tissue tumour, uterine cancer, penile cancer, prostate cancer, chronic or acute leukaemia, lymphocytic lymphoma, bladder cancer, kidney cancer, ureter cancer, renal cell carcinoma, renal pelvic carcinoma, CNS tumour, primary CNS lymphoma, bone marrow tumour, brain stem nerve gliomas, pituitary adenoma, or their combination. The protein is useful as a target for screening new anticancer agents. The present sequence represents the 84-312 amino acid sequence of p38/JTV-1 protein.

SQ Sequence 229 AA;

Query Match 64.6%; Score 1069; DB 8; Length 229;
 Best Local Similarity 88.2%; Pred. No. 2.6e-101;
 Matches 202; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

Qy |||||||DADLDVTNLIQDADEPTTLATWDLNSVLGKGDKDIVINANPASPLSLVHLRLC 143
 Db 1 DADLDVTNLIQDADEPTTLATWDLNSVLGKGDKDIVINANPASPLSLVHLRLC 60

Qy 144 ERYRVSTVHTHSSVKVNPENIWKCTGEQARKQSRRHYQLGFTLWNQNVPKTMKPSVQT 203
 Db 61 EHPRVSTVHTHSSVKVNPENIWKCTGEQARKQSRRHYQLGFTLWNQNVPKTMKPSIQT 120

Qy 204 MCPIEGEGNIRFLFSLFGOKNAVLTLLISWWDIAFMOREGSESKKEKAVFNSAL 263
 Db 121 MCPIEGEGNIRFLFSLFGOKNAVLTLLISWWDIAFMOREGSESKKEKAVFNSAL 180

Qy 264 GRSPWLVGNGELTVADYLWMSLQQIGGSSGAAPTNTORMLFLGK 312
 Db 181 GRSPWLVGNGELTVADYLWMSLQQIGGSSGAAPTNTORMLFLGK 229

RESULT 7
 ADR86552
 ID ADR86552 standard; protein; 161 AA.
 AC ADR86552;
 XX
 DT 18-NOV-2004 (first entry)
 XX

DE 1-161 amino acid sequence of p38/JTV-1 protein.
 XX
 p38/JTV-1; Cytostatic; cancer; leukemia; anticancer.
 XX
 OS Homo sapiens.
 XX
 PN EP1454628-A2.
 XX
 PR 08-SEP-2004.
 XX
 PR 09-SEP-2003; 2003EP-00020344.
 XX
 PR 03-MAR-2003; 2003KR-00013058.
 XX
 PA (UYSE-) UNIV SEOUL NAT IND FOUND.
 XX
 PI Kim S., Park B;
 XX
 DR WPI; 2004-627822/61.
 DR N-PSDB; ADR86549.
 XX
 PT New isolated p38/JTV-1 protein, useful as medicament for treating cancer e.g., stomach, liver, blood, bone, pancreatic, skin, head or neck cancer and cutaneous or intracocular melanoma, as well as for screening new anticancer agentB.

CC
 Claim 5; SEQ ID NO 5; 47pp; English.

The present invention relates to an isolated p38/JTV-1 protein for use as medicament. The p38/JTV-1 protein or the pharmaceutical composition is useful as medicament for treating breast cancer, large intestinal cancer, lung cancer, small cell lung cancer, stomach cancer, liver cancer, blood cancer, bone cancer, pancreatic cancer, skin cancer, head or neck cancer, cutaneous or intracocular melanoma, uterine carcinoma, ovarian cancer, rectal cancer, anal cancer, colon cancer, fallopian tube carcinoma, endometrial carcinoma, cervical cancer, vulval cancer, vaginal carcinoma, Hodgkin's disease, esophageal cancer, small intestine cancer, endocrine cancer, thyroid cancer, parathyroid cancer, adrenal cancer, soft tissue tumour, uterine cancer, penile cancer, prostate cancer, chronic or acute leukaemia, lymphocytic lymphoma, bladder cancer, kidney cancer, ureter cancer, renal cell carcinoma, renal pelvic carcinoma, CNS tumour, primary CNS lymphoma, bone marrow tumour, brain stem nerve gliomas, pituitary adenoma, or their combination. The protein is useful as a target for screening new anticancer agents. The present sequence represents the 1-161 amino acid sequence of p38/JTV-1 protein.

SQ Sequence 161 AA;

Query Match 44.4%; Score 735; DB 8; Length 161;
 Best Local Similarity 88.8%; Pred. No. 4.4e-67;
 Matches 143; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MPWYQVRYHGGSAPLRLPELPTCMYRLPNVHSKTTSBATDAGHQETSEPSIQALRSQD 60
 Db 1 MPWYQVRYHGGSAPLRLPELPTCMYRLPNVHSKTTSBATDAGHQETSEPSIQALRSQD 60

Qy 61 DILKRLYELKAVDGLSKMHTPPADDLVTNLQADEPTLAATNTLUDLNSYGKDGALK 120
 Db 61 DILKRLYELKAVDGLSKMHTPPADDLVTNLQADEPTLAATNTLUDLNSYGKDGALK 120

Qy 121 DIVINANPASPLSLVHLRLCERYRLSTVHTHSSVKV 161
 Db 121 DIVINANPASPLSLVHLRLCERYRLSTVHTHSSVKV 161

RESULT 8
 ABR01502
 ID ABR01502 standard; protein; 51 AA.
 AC ABR01502;
 XX
 DT 24-JUN-2002 (first entry)
 XX

DE Human ORFX protein sequence SEQ ID NO:2986.

XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;

KW hyperproliferative disorder; psoriasis; benign tumour; hemorrhage;

KW degenerative disorder; osteoarthritis; neurodegenerative disorder;

KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;

KW hypertension; hypothyroidism; cholesterol ester storage disease;

KW immune deficiency; immune disorder; infectious disease; thyroiditis;

KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroditis;

KW myasthenia gravis.

XX OS Homo sapiens.

XX PN WO200192523-A2.

XX PD 06-DEC-2001.

XX PF 29-MAY-2001; 2001WO-US010836.

XX PR 30-MAY-2000; 2000US-0206132P.

XX PR 29-AUG-2000; 2000US-0228716P.

XX PA (CURA-) CURAGEN CORP.

XX PI Shimkets RA, Leach MD;

XX DR WPI; 2002106308/14.

XX N-PSDB; ABN17254.

XX PT Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.

XX PS Disclosure; SEQ ID NO 2986; 103pp; English.

XX CC The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP0010 to ABP1500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hyperthyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX SQ Sequence 51 AA;

Query Match 13.1%; Score 216.5; DB 4; Length 334;

Best Local Similarity 26.0%; Pred. No. 4.8e-13; Mismatches 124; Indels 73; Gaps 9;

Matches 86; Conservative 48; Mismatches 124; Indels 73; Gaps 9;

QY 3 MYQVKPYHGSAPRLVPELPTOMYRPNV-----HSKUTSPATDAG----- 42

1 MYELKLT-----LPQFDITKLPCMYPKLNVSIAADSLASGTSAS-TSASSCCKLEARNID 57

DB 43 -----HYQETSPSLOALESRODDILKLYELKAADGLSKMIHTPD 84

QY 58 RTGRNAATCALDLSIGRQIQLKDPTASVARDKEVKLKQOLQIR----- 110

CC 85 ADLDVTMILQDAEPTTATNTIDLNVLGKQYGAIXDIVANPASPPLSVLHLILCE 144

QY 111 AGLGVCG--KIFQHTAFONG-----GLKEVPLDVINGHPFPIPYALLKNAWRN 161

Db 145 RYRVLSTVHTHSVKW-----PENLVKCFGEZARKOSRHEYOLGFTLWKVNPKTQM 197

QY 162 LYTDVVKFTHSMADIGPAAREFEAMLAKYFVNPLP-----KISVTLIWKGCHTEM 215

QY 198 KFSVQTMCPIEEGNARFLFSGQHNATLTI--IPSWDIAFMQFREGSSKEKAA 254

Db 216 ISSPTMMVPIXEVNTRYLGRVGPARYRVEGSPCLNEIDLVLDICYQLRNCNTKQVA 275

QY 215 VFSMNSALGRSPFWLNLVNLTVADVWMSVL 285

OM protein - protein search, using SW model

Run on: February 23, 2005, 13:36:20 ; Search time 17.81 Seconds
 (without alignment(s))
 1341.256 Million cell updates/sec

Title: US-10-622-817-6
 Perfect score: 1655
 Sequence: 1 MPMQVKPYHGGSAPLRLV... RWLKSCENLAPFSTALQLLK 320
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 513545 seqb, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1464	88.5	341	US-09-949-016-11312
2	1436	86.8	312	Sequence 11312, A
3	106	6.4	1512	Sequence 2, Appli
4	96.5	5.8	1440	Sequence 48, Appli
5	90.5	5.5	3	Sequence 37, Appli
6	90	5.4	559	Sequence 2, Appli
7	90	5.4	559	Sequence 10, Appli
8	90	5.4	2954	Sequence 4, Appli
9	90	5.4	2954	Sequence 1, Appli
10	89	5.4	5215	Sequence 2, Appli
11	89	5.4	1056	Sequence 29, Appli
12	89	5.4	1057	Sequence 10, Appli
13	89	5.4	1057	Sequence 10, Appli
14	89	5.4	1287	Sequence 7825, Ap
15	88	5.3	4	Sequence 2, Appli
16	88	5.3	1057	Sequence 29, Appli
17	88	5.3	4	Sequence 10, Appli
18	86.5	5.2	520	Sequence 10, Appli
19	86.5	5.2	967	Sequence 10, Appli
20	86	5.2	535	Sequence 10, Appli
21	85.5	5.2	85.5	Sequence 10, Appli
22	85.5	5.2	608	Sequence 10, Appli
23	85.5	5.2	657	Sequence 10, Appli
24	85	5.1	222	Sequence 10, Appli
25	85	5.1	302	Sequence 10, Appli
26	85	5.1	4	Sequence 10, Appli
27	85	5.1	1971	Sequence 1, Appli

ALIGNMENTS

```

RESULT 1
US-09-949-016-11312
; Sequence 11312, A
; Parent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIORITY APPLICATION NUMBER: 60/241, 755
; PRIORITY FILING DATE: 2000-10-20
; PRIORITY APPLICATION NUMBER: 60/237, 768
; PRIORITY FILING DATE: 2000-10-03
; PRIORITY APPLICATION NUMBER: 60/231, 498
; PRIORITY FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 11312
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11312

Query Match Best Local Similarity 88.5%; Score 1464; DB 4; Length 341;
Matched 279; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

OY 1 MPMQVKPYHGGSAPLRLVPLPCTMYRUPNVHSKTTSPATDGHVOETSSEPSLQLESROD 60
Db 22 MEMYQVKPYHGGSAPLRLVPLPCTMYRUPNVHSKTTSPATDGHVOETSSEPSLQLESROD 81
Db 22 DIVINANFASPPSLVLHLRCYRKLSTTHSSYKVNPENLVKRGEQARKQSRE 180
Db 61 DIKLKLYELKAADVGLSKMHTPDAADLVNTLQADEPTTLATNTLDNSVCKDYGALK 120
Db 82 DIKLKLYELKAADVGLSKMHTPDAADLVNTLQADEPTTLT'NALDLSVCKDYGALK 141
Db 121 DIVINANFASPPSLVLHLRCYRKLSTTHSSYKVNPENLVKRGEQARKQSRE 180
Db 142 DIVINANFASPPSLVLHLRCYRKLSTTHSSYKVNPENLVKRGEQARKQSRE 201
Db 181 YOLGFTLWQKPKTOMKPSWOTMCPTGEENGNTARFLPSLFGOKHNAVTLLTSDWDIA 240
Db 202 YOLGFTLWQKPKTOMKPSWOTMCPTGEENGNTARFLPSLFGOKHNAVTLLTSDWDIA 261
Db 241 WPLQLEGSSEKKAFAVFRSMNSNAGRSPLWGNBLTVADWVLSVLPQGGSSAAPTWNQ 300
Db 262 IFLQKEGSSKKEAVFRSMNSNAGKSPWLAGNLBTADWVLSVLPQIGGCSVTPANVO 321
QY 301 RWLKSCENLAPFSTALQLLK 320

```

Db 322 RWMRSCENLA[PNTALKLK 341

RESULT 2

; Sequence 2, Application US/08518862C
; Patent No. 5843757
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Nicolaides, Nicholas C.
; TITLE OF INVENTION: Human JTVI Gene Overlaps PMS2 Gene
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/518,862C
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Kazar, Sarah A.
; REGISTRATION NUMBER: 32, 141
; REFERENCE/DOCKET NUMBER: 01107.49697
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULAR TYPE: protein
; US-08-518-862C-2

Query Match 86.9%; Score 1436; DB 2; Length 312;
Best Local Similarity 87.5%; Pred. No. 9.6e-150;
Matches 273; Conservative 14; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MPMYQVQYHGSAPARLVEPLTOMYRPNVISRTSPATDAGHVOETSEPSIQALESRQD
1 MPWYQVQYHGSAPARLVEPLTOMYRPNVISRTSPATDAGHVOETSEPSIQALESRQD 60

Db 61 DILKRYELKAAVDGSKWMTTPDADLDTNTQDADPTTAATNTUDNSVLGKOGYALK 120

Qy 121 DIVINANPASPPLSLVTHRLICERYVTSTVHTHSSVKPVNPENLKCFCGQARKQSRE 180

Db 121 DIVINANPASPPLSLVTHRLICERYVTSTVHTHSSVKPVNPENLKCFCGQARKQSRE 180

Qy 181 YOLGFLTIWKVPTKOMKESTQMCIEGEANIARLFSJEGOKAHAVTLLISWVIA 240

Db 181 YOLGFLTIWKVPTKOMKESTQMCIEGEANIARLFSJEGOKAHAVTLLISWVIA 240

Qy 241 MFQLRBGSKEKGAVRSMSALGRSPWLWVNELTVADWVWLSVQQTGSSGAAPNTY 300

Db 241 MFQLRBGSKEKGAVRSMSALGRSPWLWVNELTVADWVWLSVQQTGSSGAAPNTY 300

301 RWLKSCENLAPF 312

301 RWLKSCENLAPF 312

RESULT 3

; Sequence 48, Application US/09443184A
; Patent No. 6372431
; GENERAL INFORMATION:
; APPLICANT: Cunningham, Mary Jane
; APPLICANT: Zweiger, Gary
; APPLICANT: Kaser, Matthew R.
; APPLICANT: Panzer, Scott
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Yue, Henry
; APPLICANT: Baughn, Mariah
; APPLICANT: Arizmaz, Yalda
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: MAMMALIAN TOXICOLOGICAL RESPONSE MARKERS
; FILE REFERENCE: PCT-007 US
; CURRENT APPLICATION NUMBER: US/09/443,184A
; CURRENT FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 138
; SEQ ID NO 4
; LENGTH: 1512
; SOFTWARE: PERL Program
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6372431 2302721CD1

US-09-443-184-48

Query Match 6.4%; Score 106; DB 3; Length 1512;
Best Local Similarity 21.8%; Pred. No. 0.096; Matches 44; Conservative 33; Mismatches 69; Indels 56; Gaps 8;

Qy 124 INANPASPPLSLVTHRLICERYVTSTVHTHSSVKPVNPENLKCFCGQARKQSRE 183

Db 6 LTWNSGDPPIGALL-----AVENHKDD-VSIVEEGENILH--- 41

Qy 184 GFTLTWKVNPRTKOMKFWSQTMCPIEGENIARFL----FSLFGQKRNAAVTLIDSWV 237

Db 42 ---VSENVIFTDV-----MSILRYLARVATTAGLYGS--NLMEITEIDHWL 82

Qy 238 DIAMFOLRGSSKKEKAVERFSMNSALGKSPWLWGNELTVADWVWLSVQ---OTGSS 292

Db 83 EFSATKL--SSCDSFTSTINELNHLCSIRTYLVGNSLISLADLCWATLKGNAWOBQLQ 140

Qy 293 GAAPINWQWLKSENLA[PFT 314

Db 141 KKAPVHVKWGFLEAQQAFOQ 162

RESULT 4

US-09-357-251-37

; Sequence 37, Application US/09357251
; Patent No. 6271441
; GENERAL INFORMATION:
; APPLICANT: Falco, S. Carl
; APPLICANT: Famodu, Dayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Schwaber, James S.
; TITLE OF INVENTION: Plant Aminoacyl-tRNA Synthetase
; FILE REFERENCE: BB-1193
; CURRENT APPLICATION NUMBER: US/09/357,251
; CURRENT FILING DATE: 1999-07-20
; EARLIER APPLICATION NUMBER: 60/093,530
; EARLIER FILING DATE: July 21, 1998
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 37
; LENGTH: 1440
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-357-251-37

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: February 23, 2005, 13:57:26 ; Search time 50.2443 Seconds

Perfect score: 1655 ; Sequence: MPMYQVTPYHGGSAAPRLVEL...; (without alignments)
Sequence: RNLKSCENLAPFETALQLLK 320 ; 2084.158 Million cell updates/sec

Title: US-10-622-817-6
Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5

Searched: 1380268 seqs, 32721040 residues

Total number of hits satisfying chosen parameters: 1380168

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0% ; Maximum Match 100% ; Listing first 45 summaries

Database : Published Applications AA:
1: /cgnd_6/prodata/1/pubpaas/us07_PUBCOMB.pep:*

2: /cgnd_6/prodata/1/pubpaas/PCTN_PUBCOMB.pep:*

3: /cgnd_6/prodata/1/pubpaas/us06_PUBCOMB.pep:*

4: /cgnd_6/prodata/1/pubpaas/us06_PUBCOMB.pep:*

5: /cgnd_6/prodata/1/pubpaas/us07_PUBCOMB.pep:*

6: /cgnd_6/prodata/1/pubpaas/us08_PUBCOMB.pep:*

7: /cgnd_6/prodata/1/pubpaas/us08_PUBCOMB.pep:*

8: /cgnd_6/prodata/1/pubpaas/us09_PUBCOMB.pep:*

9: /cgnd_6/prodata/1/pubpaas/us09_PUBCOMB.pep:*

10: /cgnd_6/prodata/1/pubpaas/us09_PUBCOMB.pep:*

11: /cgnd_6/prodata/1/pubpaas/us09c_PUBCOMB.pep:*

12: /cgnd_6/prodata/1/pubpaas/us09c_PUBCOMB.pep:*

13: /cgnd_6/prodata/1/pubpaas/us10_PUBCOMB.pep:*

14: /cgnd_6/prodata/1/pubpaas/us10c_PUBCOMB.pep:*

15: /cgnd_6/prodata/1/pubpaas/us10c_PUBCOMB.pep:*

16: /cgnd_6/prodata/1/pubpaas/us10c_PUBCOMB.pep:*

17: /cgnd_6/prodata/1/pubpaas/us10c_PUBCOMB.pep:*

18: /cgnd_6/prodata/1/pubpaas/us11c_PUBCOMB.pep:*

19: /cgnd_6/prodata/1/pubpaas/us60c_PUBCOMB.pep:*

20: /cgnd_6/prodata/1/pubpaas/us60c_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
------------	-------	--------------------	-------	-------------

RESULT 1
US-10-463-676-4
; Sequence 4, Application US/10463676
; Publication No. US20040175375A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Sungsoon
; ATTORNEY: Park, Bum-Joon
; TITLE OF INVENTION: Method for Treating Cancer Using P38/JTV-1 and Method for Screening Pharmaceutical Composition for Treating Cancer
; FILE REFERENCE: 012670-091
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: KR 10-2003-13058
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: PEPTIDE
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(312)
; OTHER INFORMATION: 1-312 amino acid sequence of p38/JTV-1
US-10-463-676-4

Query Match Score 86.8%; Score 1436; DB 16; Length 312;
Best Local Similarity 87.5%; Pred. No. 2.6e-137; Length 312;
Matches 273; Conservative 14; Mismatches 25; Indels 0; Gaps 0;

QY 1 MPMYQVTPYHGGSAAPRLVELPTCMYRPNVHSKTSRPAAGHWTSPERSQLAESRQD 60
QY 1 MPYQVTPYHGGSAAPRLVELPTCMYRPNVHSKTSRPAAGHWTSPERSQLAESRQD 60
Db Sequence 5841, Ap Sequence 37, Appl Sequence 31, Appl Sequence 123904, Sequence 10013, A

QY 61 DILKRIVELKAADVGLSKMIRPDADLVNLQADEPPTLATNTIDNSVTLGKDYGALK 120

Db 61 DILKRYELKAADVDSLKMTQTPDADLVNTIQADEBPTLTNAIDLNSVLGKGALK 120

QY TITLE OF INVENTION: Method for Treating Cancer Using P38/JTV-1 and Method

Db 121 DIVINANPASPPLSLVILVHLRILCERYRLVSLVTHSSVKVNPEVNUVCFGEQARKQSRAE 180

FILE REFERENCE: 012679-091

Db 121 DIVINANPASPPLSLVILVHLRILCEHFRVLSTVHTHSSVKVNPEVNLKCFGEONKQPROD 180

CURRENT APPLICATION NUMBER: US10/463,676

Db 181 YOLGFTLWINKVPKQMKSISVOTMCPIEGGNIAARPLSLFGQKENAVITLIDSWVDTA 240

PRIOR APPLICATION NUMBER: KR 10-2003-13058

Db 181 YOLGFTLWINKVPKQMKSISVOTMCPIEGGNIAARPLSLFGQKENAVITLIDSWVDTA 240

PRIOR FILING DATE: 2003-03-03

Db 241 MFOQREGSSKEAKAVERFSMSALGSPWLWGNELTJADVLWSVLIQOQGSSGAAPTNTQ 300

NUMBER OF SEQ ID NOS: 17

SOFTARE: FastSEQ for Windows Version 4.0

Db 241 MFOQREGSSKEAKAVERFSMSALGSPWLWGNELTJADVLWSVLIQOQGSSGAAPTNTQ 300

SRQ ID NO 5

LENGTH: 161

Db 301 RWLKSCENLAPF 312

TYPE: PRT

Db 301 RWLKSCENLAPF 312

ORGANISM: Homo sapiens

FEATURE: PEPTIDE

NAME/KEY: PEPTIDE

LOCATION: (1..(161)

OTHER INFORMATION: 1-161 amino acid sequence of p38/JTV-1

US-10-463-676-5

RESULT 2

US-10-463-676-6

Sequence 6, Application US/10463676

Publication No. US20040175375A1

GENERAL INFORMATION:

Applicant: Kim, Sunghoon

Applicant: Park, Bum-Joon

Title of Invention: Method for Treating Cancer Using P38/JTV-1 and Method

Title of Invention: for Screening Pharmaceutical Composition for Treating Cancer

File Reference: 012679-091

Current Application Number: US10/463,676

Current Filing Date: 2003-06-18

Prior Application Number: KR 10-2003-13058

Prior Filing Date: 2003-03-03

Number of Seq ID Nos: 17

Software: FastSEQ for Windows Version 4.0

Seq ID No 6

Length: 229

Type: PRT

Organism: Homo sapiens

Feature:

Name/Key: PEPTIDE

Location: (1)..(229)

Other Information: 84-312 amino acid sequence p38/JTV-1

US-10-463-676-6

Query Match 44.4%; Score 735; DB 16; Length 161;

Best Local Similarity 88.8%; Pred. No. 2.5e-66;

Matches 143; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

Db 1 MPMPMQVKYHGGSAPLRLVPLPOMYLPNVRHRTSPATDAGVQETSEPSHQALESRQD 60

QY 1 MPMPMQVKYHGGSAPLRLVPLPOMYLPNVRHRTSPATDAGVQETSEPSHQALESRQD 60

Db 61 DILKRYELKAADVDSLKMTQTPDADLVNTIQADEPTTLATNTLQNSVKGDXALK 120

QY 61 DILKRYELKAADVDSLKMTQTPDADLVNTIQADEPTTLATNTLQNSVKGDXALK 120

Db 61 DILKRYELKAADVDSLKMTQTPDADLVNTIQADEPTTLATNTLQNSVKGDXALK 120

QY 121 DIVINANPASPPLSLVILVHLRILCERYRLVSLVTHSSVKVN 161

Db 121 DIVINANPASPPLSLVILVHLRILCEHFRVLSTVHTHSSVKVN 161

Db 121 DIVINANPASPPLSLVILVHLRILCEHFRVLSTVHTHSSVKVN 161

US-10-437-963-126132

RESULT 4

US-10-437-963-126132

Sequence 126132, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

Applicant: La Rosa, Thomas J.

Applicant: Kovacic, David K.

Applicant: Zhou, Yihua

Applicant: Cao, Yongwei

Applicant: Wu, Wei

Applicant: Barukharov, Andrey A.

Applicant: Barbazuk, Brad

Applicant: Li, Ping

Title of Invention: Rice Nucleic Acid Molecules and Other Molecules Associated With

Title of Invention: Plants and Uses Thereof for Plant Improvement

File Reference: 38-21(15322)B

Current Application Number: US10/437,963

Current Filing Date: 2003-05-14

Number of Seq ID Nos: 2,04966

Seq ID No 126132

Length: 925

Type: PRT

Organism: Oryza sativa

Feature:

Other Information: Clone ID: PAT-NRT4530_28709C.1.pep

US-10-437-963-126132

Query Match 6.4%; Score 105.5; DB 16; Length 925;

Best Local Similarity 20.3%; Pred. No. 0.51;

Matches 64; Conservative 46; Mismatches 107; Indels 99; Gaps 13;

Db 25 YRLDNVHSKTSPTADGHVQESSEPSIQALSERQRDDI-LAKLYELKAADVDSLKMTQ 82

QY 25 YRLDNVHSKTSPTADGHVQESSEPSIQALSERQRDDI-LAKLYELKAADVDSLKMTQ 82

Db 152 YMMDNIKAVTGVV-----TIDPRQLAYKRTTLEVGIEQSEKLUVKVLSIGDDYHA 203

QY 152 YMMDNIKAVTGVV-----TIDPRQLAYKRTTLEVGIEQSEKLUVKVLSIGDDYHA 203

Applicant: Kim, Sunghoon

Applicant: Park, Bum-Joon

Applicant: Park, Bum-Joon

GenCore version 5.1.6
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OM protein - protein search, using SW model.

Run on: February 23, 2005, 13:34:50 ; Search time 13.3213 Seconds
 (without alignments)
 2311.294 Million cell updates/sec

Title: US-10-622-817-6
Perfect score: 1655
Sequence: 1 MPMTQVQKPYHGGSAPRLVEL.....RNLKSCENLAPFSTALQQLK 320

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR 79;*
 1: pir1;*
 2: pir2;*
 3: pir3;*
 4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	126.5	7.6	719	2	Tr2043
2	112	6.8	728	2	T01200
3	104	6.3	980	2	T00089
4	99	6.0	691	2	B29799
5	98.5	6.0	222	2	G2441
6	98.5	6.0	377	2	F29172
7	98	5.9	690	2	A24545
8	96.5	5.8	1440	1	S2H0QT
9	95	5.8	753	1	T24869
10	95	5.7	488	1	H24313
11	95	5.7	552	2	D2421
12	94.5	5.7	2655	2	D26595
13	94	5.7	2471	2	T24977
14	94	5.7	435	2	T01567
15	94	5.7	436	2	Q26719
16	93.5	5.6	1064	2	B26465
17	93	5.6	490	2	D24999
18	91.5	5.6	754	2	S27403
19	91.5	5.5	436	2	I51237
20	91	5.5	1265	2	T247626
21	90.5	5.5	359	2	T37921
22	90.5	5.5	456	2	C04764
23	90.5	5.5	642	2	T24940
24	90.5	5.5	716	2	T27830
25	90	5.4	437	2	I51238
26	90	5.4	559	2	A38604
27	90	5.4	2954	2	T24156
28	89.5	5.4	317	2	T05528
29	89.5	5.4	1597	2	S25053

ALIGNMENTS

RESULT 1

152043 probable glutamate-tRNA ligase (EC 6.1.1.17) [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
 C;Accession: T22043
 R;Day, I.S.; Golovkin, M.; Reddy, A.S.
 Biochim. Biophys. Acta 1399, 219-24, 1998
 A;Title: Cloning of the cDNA for glutamyl-tRNA synthetase from *Arabidopsis thaliana*.
 A;Reference number: Z24836; MNUID:5-65600; PMID:9755600
 A;Accesion: T22043
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-719 <DLY>
 A;Cross-references: UNIPROT:OB2462; EMBL:AF067773; PIDN: AAC36469.1
 C;Superfamily: yeast glutamate-tRNA ligase; glutamine-tRNA ligase homology
 C;Keywords: ligase

Query Match 7.6%; Score 126.5; DB 2; Length 719;
 Best Local Similarity 28.0%; Pred. No. 0.017; Pred. No. 0.017;
 Matches 49; Conservative 22; Mismatches 57; Indels 47; Gaps 8;

Qy	128	PASPPILLSVHLICRYRVLSTVTHSSVKNVPNLVKCFGEQARKQSREHYQLGFTL	187
Db	10	:: <p>multifunctional amide synthetase Peptidase S-tran penicillin-binding neural zinc finger kinesin-like interphotoreceptor gtp-binding protein acetyl-CoA synthetase hypothetical protein acetyl-CoA carboxylase hypothetical protein AMP-dependent helicase hypothetical protein pre-mRNA splicing</p> <p>RESULT 2</p> <p>probable glutamate-tRNA ligase (EC 6.1.1.17) F21E10.12 - <i>Arabidopsis thaliana</i> C;Species: <i>Arabidopsis thaliana</i> (mouse-ear cress) C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004 C;Accession: T01200 C;Davidson, S.; Roiffing, T.; David, M.; O'Brian, D. submitted to the EMBL Data Library, April 1998 A;Description: The sequence of <i>A. thaliana</i> F21E10. A;Reference number: Z14258 A;Accession: T01200 A;Status: translated from GB/EMBL/DDJB A;Molecule type: DNA A;Residues: 1-728 <DAV> A;Cross-references: UNIPROT:OB65253; EMBL:AF058914; NID:93047074; PID:93047084; GSPDB:GN0 A;Experimental source: cultivar Columbia C;Genetics:</p>	

A;Gene: ATSP:F21P10.12
A;Map position: 5
A;Introns: 47/2; 89/3; 141/1; 503/3; 659/3
C;Superfamily: yeast glutamate-tRNA ligase; glutamine-tRNA synthetase; ligase; protein biosynthesis
C;Keywords: aminoacyl-tRNA synthetase; glutamine-tRNA ligase homology <BGL>
F:223-499/bdomain: glutamine-tRNA ligase homology <BGL>

Query Match 6.8%; Score 112; DB 2; Length 728;
Best Local Similarity 26.6%; Pred. No. 0, 29; Mismatches 57; Indels 56; Gaps 9;
Matches 49; Conservative 22; Mismatches 57; Indels 56; Gaps 9;

QY 128 PASPPSILVILURLLCERYRVLSTVHSSKVNPRLVKRGAFKRSKHEYQIQLGFTL 187
Db 10 PESPPSVIVALSASPV---TIDSSAAATTVPSPVF---SDQRKLN----GATV 55
Db 56 LIRYY-----GRAKKLDIFYG--NNADFSQSVLICINMKIDEWVD 95
Db 239 IAMFOQREGSSKEKAAVFRSMNSALGRSPWPMVGNETIVDQVLMSTLQQQGGSSGAAPTN 298
Db 96 YASV_PSSGSFENAC_GRDVKYLESTFLVGHSLSIADVAINSLAGTG-----143
QY 299 VORW 302
Db 144 -QRW 146

RESULT 3
T30089
probable zinc proteinase (EC 3.4.24.-) C02G6.1 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30089
R;Bentley, D.; Kemp, K.; Scheetz, P.
submitted to the EMBL Data library, April 1996
A;Description: The sequence of *C. elegans* cosmid C02G6.
A;Reference number: 220734
A;Accession: T30089
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-980 <BEN>
A;Experimental source: strain Bristol N2; clone C02G6
A;Gene: CESP:C02G6.1
A;Map position: 5
A;Introns: 25/3; 215/2; 266/3; 540/3; 585/3; 786/1; 898/2
C;Keywords: hydrolase; metalloproteinase; zinc
C;Genetics:
F:/73/Active site: Glu #status predicted

Query Match
Best Local Similarity 6.0%; Score 99; DB 2; Length 691;
Matches 65; Conservative 53; Pred. No. 3.4; Mismatches 110; Indels 94; Gaps 15;
Matches 65; Conservative 53; Mismatches 110; Indels 94; Gaps 15;

QY 1 NPMWQKPKHGGASPLRVELPTCMYRLPNVHSKTSPTAD-----GHVQETSEPSL 52
Db 172 IPAQVYLPNHDQKAPTPSTRPS-----NDKAPKSKTKAQDATTDKHPIQNQDTHQPAH 223
Db 53 QALQESODDIKKLVELKAADGJSKMI--HTPABDL-----VNLQDDEPTTL 101
Db 224 QIDAKQDPV-RQSBQKPRQVGDSLKHIDQNSPBKPTDKTDQKLIKDALQ-A-PKTR 280
QY 102 ATNTDLDINSVIGKDYGALKDQIVINANPASPPLSLVHLILCEYRVLSTVHSSKV 161
Db 281 STTMIAAD-----AKKVPRPLKANQVP-----LNKYPV---VFVHGFLIGV 318
Db 162 PENLWKGFG-----EQARKQSREYQLGFTLWIKNVFK-TOMKFSVQTMCPTEG 209
Db 319 GDNAPALPYNPGSGNKFKVYIEELLKQGVNVHQASAFGSNVYRAVEVYVYIKGRDVYD 378
QY 210 EGNAFLPSLFGOKHNAV-----TTLTIDSWDIDAMFOURBESS 249
Db 379 AAHHAKYGHERRYGKTYKGJMPNWPGKKVHLVGHISMGGQTIRLMEF-----LRNG-N 430
QY 250 KEKAVALFRSMNSALGRSPWLVG 271
Db 431 KEEIAVHRANGGET-SPLFTG 450

RESULT 4
B89797
glycerol ester hydrolase [Imported] - *Staphylococcus aureus* (strain N315)
C;Species: *Staphylococcus aureus*
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: B89797
R;Kuroda, M.; Oha, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; Lancet, 357, 1225-1240, 2001.
A;Title: Whole genome sequencing of meticillin-resistant *Staphylococcus aureus*.
A;Reference number: A89750; MUID:21311952; PMID:1418146
A;Accession: B89797
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-691 <KUR>
A;Cross-references: UNIPROT:Q99W06; GB:BA000018; PID:913700235; PIDN:BAB41533.1; GSPDB:6
A;Experimental source: strain N315
C;Genetics:
C;Gene: gen
C;Superfamily: *Staphylococcus* triacylglycerol lipase

Query Match
Best Local Similarity 6.0%; Score 99; DB 2; Length 691;
Matches 65; Conservative 53; Pred. No. 3.4; Mismatches 110; Indels 94; Gaps 15;
Matches 65; Conservative 53; Mismatches 110; Indels 94; Gaps 15;

QY 1 NPMWQKPKHGGASPLRVELPTCMYRLPNVHSKTSPTAD-----GHVQETSEPSL 52
Db 172 IPAQVYLPNHDQKAPTPSTRPS-----NDKAPKSKTKAQDATTDKHPIQNQDTHQPAH 223
Db 53 QALQESODDIKKLVELKAADGJSKMI--HTPABDL-----VNLQDDEPTTL 101
Db 224 QIDAKQDPV-RQSBQKPRQVGDSLKHIDQNSPBKPTDKTDQKLIKDALQ-A-PKTR 280
QY 102 ATNTDLDINSVIGKDYGALKDQIVINANPASPPLSLVHLILCEYRVLSTVHSSKV 161
Db 281 STTMIAAD-----AKKVPRPLKANQVP-----LNKYPV---VFVHGFLIGV 318
Db 162 PENLWKGFG-----EQARKQSREYQLGFTLWIKNVFK-TOMKFSVQTMCPTEG 209
Db 319 GDNAPALPYNPGSGNKFKVYIEELLKQGVNVHQASAFGSNVYRAVEVYVYIKGRDVYD 378
QY 210 EGNAFLPSLFGOKHNAV-----TTLTIDSWDIDAMFOURBESS 249
Db 379 AAHHAKYGHERRYGKTYKGJMPNWPGKKVHLVGHISMGGQTIRLMEF-----LRNG-N 430
QY 250 KEKAVALFRSMNSALGRSPWLVG 271
Db 431 KEEIAVHRANGGET-SPLFTG 450

RESULT 5
G8241
probable glutathione S-transferase VCA0584 [Imported] - *Vibrio cholerae* (strain N16961 ssp. *cholerae*)
446 KMKYEVALKITSHHALLPPEK-N-EVATNGQKPKRSVKEHPLKISDDGWSRWTKF 503

Query Match 100.0%; Score 1655; DB 2; Length 320;
 Best Local Similarity 100.0%; Pred. No. 2.6e-128; DR
 Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPMYQVKPVHGGSPALPVELPTCMYLPNWHSKTSPATDAGHVOESEPSIQALESQD 60
 1 MPMYQVKPVHGGSPALPVELPTCMYLPNWHSKTSPATDAGHVOESEPSIQALESQD 60

Db 61 DILKRYELKAVADGLSKMHTPDADLYNLQADEPTTLATNTLIDSVAGKDYGALK 120
 61 DILKRYELKAVADGLSKMHTPDADLYNLQADEPTTLATNTLIDSVAGKDYGALK 120

QY 121 DIVINANPASPLSLVHLRLCERYRVLSTVTHSSVKNVPENLVKCFGEQARKSRE 180
 121 DIVINANPASPLSLVHLRLCERYRVLSTVTHSSVKNVPENLVKCFGEQARKSRE 180

Db 181 YOLGFTLTIWKNVKPDKOMFSVOTMCPIEGEIGNARFLSLFSGOKHNAVTLLSDWIDIA 240
 181 YOLGFTLTIWKNVKPDKOMFSVOTMCPIEGEIGNARFLSLFSGOKHNAVTLLSDWIDIA 240

QY 241 MFQREGSSKEKAUVFRNSMSALGRSPMLVGNELTVAUWLWSVLOOTGGSSAAPTIVQ 300
 241 MFQREGSSKEKAUVFRNSMSALGRSPMLVGNELTVAUWLWSVLOOTGGSSAAPTIVQ 300

Db 301 RWLKSCENLAPESTALQLIK 320
 301 RWLKSCENLAPESTALQLIK 320

RESULT 2

Q8R2Y6 PRELIMINARY; PRT; 320 AA.

ID Q8R2Y6 AC 08R2Y6; GN OS OC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Murida; Murine; Mus. RN [1]— Jtv1-pending protein.
 Name=Jtv1;

DT DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DR RPK—SEQUENCE FROM N.A.

RC STRAIN=CZECH II; TISSUE=Mammary tumor; MEDLINE=22382827; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Hopkins R.F., Peingold B.A., Grouse I.H., Derge J.G.,
 Altschul S.F., Zeeberg B., Bustein K.H., Scheuer C.F.,
 Strausberg R.L., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Maruyama K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetetz T.B.,
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Milbury S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay J.J., Hulyk S.W.,
 Villalon D.K., Muzyk D.M., Sodergren E.J., Lu X., Gibbs R.K.,
 Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,
 Krzywinski M.I., Skalska U., Smailus D.E., Schniech A., Schein J.E.,
 Jones S.J., Mazra M.A.; Generation and initial analysis of more than 15,000 full-length human
 RT mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2] SEQUENCE FROM N.A.

RP STRAIN=CZECH II; TISSUE=Mammary tumor;

RA Strausberg R.; Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC026958; AAH26958.1; -

DR MGD; MGI:2385237; JEv1.

DR InterPro; IPR004046; GST_Cterm.

DR InterPro; IPR010987; GST_C_like.

DR Pfam; PF00043; GST_C; 1;

SQ SEQUENCE 320 AA; 35423 MW; 1C21F1A74C9882B4 CRC64;

Query Match 99.8%; Score 1652; DB 2; Length 320;
 Best Local Similarity 99.7%; Pred. No. 4.6e-128; DR
 Matches 319; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPMYQVKPVHGGSPALPVELPTCMYLPNWHSKTSPATDAGHVOESEPSIQALESQD 60
 1 MPMYQVKPVHGGSPALPVELPTCMYLPNWHSKTSPATDAGHVOESEPSIQALESQD 60

Db 61 DILKRYELKAVADGLSKMHTPDADLYNLQADEPTTLATNTLIDSVAGKDYGALK 120
 61 DILKRYELKAVADGLSKMHTPDADLYNLQADEPTTLATNTLIDSVAGKDYGALK 120

QY 121 DIVINANPASPLSLVHLRLCERYRVLSTVTHSSVKNVPENLVKCFGEQARKSRE 180
 121 DIVINANPASPLSLVHLRLCERYRVLSTVTHSSVKNVPENLVKCFGEQARKSRE 180

Db 181 YOLGFTLTIWKNVKPDKOMFSVOTMCPIEGEIGNARFLSLFSGOKHNAVTLLSDWIDIA 240
 181 YOLGFTLTIWKNVKPDKOMFSVOTMCPIEGEIGNARFLSLFSGOKHNAVTLLSDWIDIA 240

QY 241 MFQREGSSKEKAUVFRNSMSALGRSPMLVGNELTVAUWLWSVLOOTGGSSAAPTIVQ 300
 241 MFQREGSSKEKAUVFRNSMSALGRSPMLVGNELTVAUWLWSVLOOTGGSSAAPTIVQ 300

Db 301 RWLKSCENLAPESTALQLIK 320
 301 RWLKSCENLAPESTALQLIK 320

RESULT 3

MCA2_CRGCR ID MCA2_CRGCR STANDARD; PRT; 320 AA.

AC 09WWT7; DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)

DB Multisynthetase complex auxiliary component p38.

OS Crictellulus griseus (Chinese hamster).

OC Bokaryota; Mammalia; Eutheria; Rodentia; Sciurognathi; Murida; Cricetinae;
 OC Crictellulus.

OX NCBI_TaxID=1029; RN [1]— Jtv1-pending protein.
 RP SEQUENCE FROM N.A.

RC TISSUE=Ovary; MEDLINE=99056915; PubMed=9878398; DOI=10.1006/jmbi.1998.2316;

RA Quevillon S., Robinson J.-C., Berthonneau E., Siatecka M., Mirande M.;
 RA "Macromolecular assemblage of aminoacyl-tRNA synthetases: identification of protein-protein interactions and characterization of a core protein," J. Mol. Biol. 285:183-195 (1999).

CC — FUNCTION: Probable core protein of the multisynthetase complex which serves as a template for the assembly of the supramolecular structure.

CC — SUBUNIT: Component of the multisynthetase complex which is comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, the monospecific isoleucyl, leucyl, glutamyl, methionyl, lysyl, arcyanyl, and aspartyl-tRNA synthetases as well as three auxiliary proteins, p18, p48 and p43.

CC — SIMILARITY: Contains 1 GST-like domain.

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CC or send an email to license@sb-sib.ch).

Query Match 95.0%; Score 1573; DB 1; Length 320;
Bert Local Similarity 94.4%; Pred. No. 1.6e-121; Indels 0; Gaps 0;
Matches 302; Conservative 6; Mismatches 12; Indels 0; Gaps 0;
SEQUENCE 320 AA; 35433 MW; 6D24E033ABC810A CRC64;

QY 1 NPMYQVKPVHGSAPLRLVPLTCMRYLPUVNSKTSPTADGHVQETSEPSIQLAESRQD 60
1 NPMYQVKPVHGSAPLRLVPLTCMRYLPUVNSKTSPTADGHVQETSEPSIQLAESRQD 60

QY 61 DILKRYELKAVADGLSKMHTPDAVLVNLQADEPTTAATNTLDSLNLVLGKOGALK 120
61 DILKRYELKAVADGLSKMHTPDAVLVNLQADEPTTAATNTLDSLNLVLGKOGALK 120

Db 121 DIVINANPASPLSLVHLRLLCERYRLVSTVHTHSVKVNUPENLVICFGQEARQSRHE 180
121 DIVINANPASPLSLVHLRLLCERYRLVSTVHTHSVKVNUPENLVICFGQEARQSRHE 180

QY 181 YOLGFTLIWKVNPKTOMKFSQTMCPIEGENIARLFLSFQGKHNWVTLIDSWDIA 240
181 YOLGFTLIWKVNPKTOMKFSQTMCPIEGENIARLFLSFQGKHNWVTLIDSWDIA 240

QY 241 NFOLEGSSKEKAVERSMUSALGRSPWLVQELTVADWVLSVQQTGSAGPAVTNQ 300
241 NFOLEGSSKEKAVERSMUSALGRSPWLVQELTVADWVLSVQQTGSAGPAVTNQ 300

Db 301 RWLKGCENTLPRTAQLK 320
301 RWLKGCENTLPRTAQLK 320

Db

RESULT 4

MCA2_HUMAN STANDARD; PRT; 320 AA.

ID MCA2_HUMAN STANDARD; PRT; 320 AA.

AC Q1155; OSPII2; 35, Created)

DT 01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)

DE Multisynthetase complex auxiliary component p38 (JTV-1 protein) (PRO092).

DE Name=JTV-1;

DE Homo_sapiens (Human); Chordata; Craniata; Vertebrata; Euteleostomi; OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; OX NCBI_TaxID=9606; [1]

RN SEQUENCE FROM N.A.

RP MEDLINE-96115882; PubMed-8666379;

RA Niclaidis N.C., Kintzler K.W., Vogelstein B.; "Analysis of the 5' region of PMS2 reveals heterogeneous transcripts and a novel overlapping gene."; RT Genomics 29:329-334(1995).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Lymph;

RX MEDLINE-22388357; PubMed-12477932; DOI=10.1073/pnas.240603899;

RA Strauberg R.L., Ringold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Sheinman C.M., Schuler G.D., Altchul S.F., Zeeberg B., Buetow K.H., Scheuer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Maruyama K., Farmer A.R., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetzke T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Caminchi P., Prange C., Brown S.S., Loqueland N.A., Petersen G.J., Abramson R.D., Mulahy S.J., Bosak P.J., McKenna N.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Keightman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinwood J., Schmitz J., Myers R.M., Butterfield Y.S.N., Krzyniak M.T., Schatz J., Smailus D.E., Schnarch A., Schein J.E., Jones S.J.M., Marra M.A., Stalska U., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RR [3]

RR SEQUENCE OF 197-320 FROM N.A.

RR TISSUE=Fetal liver;

RR Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Ouyang S., Luo L., Bi J., Liu M., He F.; "Functional prediction of the coding sequences of 121 new genes deduced by analysis of cDNA clones from human fetal liver.," Submitted (DEG1998) to the EMBL/GenBank/DBJ databases.

RR [4]

RR INTERACTION WITH FUBP1; MEDLINE=22716900; PubMed=12819782; DOI=10.1038/ng1182; RAX Kim M.J., Park B.-J., Kang Y.-S., Kim H.J., Park J.-H., Kang J.W., Lee S.W., Han J.M., Lee H.-W., Kim S.; "Downregulation of FUBP1-binding protein and c-myc by tRNA synthetase cofactor p38 is required for lung cell differentiation.," Nat. Genet. 34:330-336 (2003).

CC -!- FUNCTION: Probable core protein of the multisynthetase complex that serves as a template for the assembly of the supramolecular structure. Mediates ubiquitination of FUBP1 and its degradation by the proteasome.

CC -!- SUBUNIT: Component of the multisynthetase complex which is comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, the monospecific isoleucyl-leucyl-glutaminyl, methionyl, lysyl, arginyl, and aspartyl-tRNA synthetases as well as three auxiliary proteins, p18, p48 and p13. Bands FUBP1.

CC -!- SIMILARITY: Contains 1 GST-like domain.

CC -!- CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 312.

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CC DR EMBL: U24169; AAC0391-1; ALT FRAME.

CC DR EMBL: BC002853; AAC02853_1; -.

CC DR EMBL: BC010156; AAC10156_1; -.

CC DR EMBL: AF116615; AACF116615_1; -.

CC DR INVDB; HKX006460; -.

CC MIH; 600859; -.

CC DR InterPro: IPR010987; GST_C_like.

CC DR InterPro: IPR00446; GST_Cterm.

CC DR Pfam; PF00043; GST_C; 1.

CC Protein biosynthesis.

SQ SEQUENCE 320 AA; 35349 MW; F253726B63C12BAB CRC64;

Query Match 88.5%; Score 1464; DB 1; Length 320;
Bert Local Similarity 87.2%; Pred. No. 1.6e-112; Indels 0; Gaps 0;
Matches 279; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY 1 NPMYQVKPVHGSAPLRLVPLTCMRYLPUVNSKTSPTADGHVQETSEPSIQLAESRQD 60
1 NPMYQVKPVHGSAPLRLVPLTCMRYLPUVNSKTSPTADGHVQETSEPSIQLAESRQD 60

Db 61 DILKRYELKAVADGLSKMHTPDAVLVNLQADEPTTAATNTLDSLNLVLGKOGALK 120
61 DILKRYELKAVADGLSKMHTPDAVLVNLQADEPTTAATNTLDSLNLVLGKOGALK 120

QY 61 DILKRYELKAVADGLSKMHTPDAVLVNLQADEPTTAATNTLDSLNLVLGKOGALK 120
61 DILKRYELKAVADGLSKMHTPDAVLVNLQADEPTTAATNTLDSLNLVLGKOGALK 120

QY 121 DIVINANPASPLSLVHLRLLCERYRLVSTVHTHSVKVNUPENLVICFGQEARQSRHE 180
121 DIVINANPASPLSLVHLRLLCERYRLVSTVHTHSVKVNUPENLVICFGQEARQSRHE 180

Db	5	QETSEPSLQALESRQDIDKRYELKAADVDSLKMHTPDAADDLVNLQADEPTLATN	QY	1 MPMYQKPKYHGGASPLRVELTOMYRLPNVHSKTSPPATDAGHVQETSEPSLQALESRQD
Db	105	TLDLNSTLGKOGALDVTINANPAPLSPSLVLHULCERYRVLTVTHSSVKOPEN	QY	1 MPMYQKPKYHGGASPLRVELTOMYRLPNVHSKTSPPATDAGHVQETSEPSLQALESRQD
Db	65	TLDLNSTLGKOGALDVTINANPAPLSPSLVLHULCERYRVLTVTHSSVKOPEN	QY	1 MPMYQKPKYHGGASPLRVELTOMYRLPNVHSKTSPPATDAGHVQETSEPSLQALESRQD
Db	65	TLDLNSTLGKOGALDVTINANPAPLSPSLVLHULCERYRVLTVTHSSVKOPEN	QY	1 MPMYQKPKYHGGASPLRVELTOMYRLPNVHSKTSPPATDAGHVQETSEPSLQALESRQD
Db	165	LVKCFGEQARQSRHEVOLGFTLIWKVNPVKQOMKFSVOTMCPIEGEGRNIAPLFLSFQOK	QY	1 MPMYQKPKYHGGASPLRVELTOMYRLPNVHSKTSPPATDAGHVQETSEPSLQALESRQD
Db	125	LVKCFGEQARQSRHEVOLGFTLIWKVNPVKQOMKFSVOTMCPIEGEGRNIAPLFLSFQOK	QY	1 MPMYQKPKYHGGASPLRVELTOMYRLPNVHSKTSPPATDAGHVQETSEPSLQALESRQD
Qy	225	HNAVTLLIDWVNDIANFOLRGSSKEKAAPFRMSMALSALGSPWLVCNELTIVADVLWSV	QY	1 MPMYQKPKYHGGASPLRVELTOMYRLPNVHSKTSPPATDAGHVQETSEPSLQALESRQD
Db	185	HNAVTLLIDWVNDIANFOLRGSSKEKAAPFRMSMALSALGSPWLVCNELTIVADVLWSV	QY	1 MPMYQKPKYHGGASPLRVELTOMYRLPNVHSKTSPPATDAGHVQETSEPSLQALESRQD
Qy	285	IQQTGESSGGAAPTNVORWLKSCENLAPPSTALQLK 320	QY	1 MPMYQKPKYHGGASPLRVELTOMYRLPNVHSKTSPPATDAGHVQETSEPSLQALESRQD
Db	245	IQQTGESSGGAAPTNVORWLKSCENLAPPSTALQLK 280	QY	1 MPMYQKPKYHGGASPLRVELTOMYRLPNVHSKTSPPATDAGHVQETSEPSLQALESRQD
RESULT 7				
Q6DK86		PRELIMINARY;	PRT;	311 AA.
ID	Q6DK86			
AC	Q6DK86;			
DT	25-OCT-2004 (TREMBLrel. 28, Created)			
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)			
DR	MGC6221 protein.			
GN	Name=MGC6221;			
OS	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;			
OX	Xenopus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Embryo;			
RX	Medline=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klaunier R.D., Collins F.S., Wagner L., Shevchenko C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Schuler G.D.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko C., Prange C.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzyniak M.I., Skalska U., Smajlous D.B., Schnurch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human",			
RT	and mouse cDNA sequences", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RC	TISSUE=Embryo;			
RA	Klein S., Gerhard D.S.; Submitted (JUN 2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC074561; AAH74561_1; -;			
DR	InterPro; IPR004046; GST_Ctern.			
DR	InterPro; IPR010987; GST_C_like.			
DR	PFam; PF00043; GST_C_1.			
SEQUENCE	311 AA; 34480 MW; D98F27F3C466154 CRC64;			
Query Match	69.7%; Score 1153.5; DB 2; Length 311;			
Best Local Similarity	67.5%; Fred. No. 6.8e-67;			
Matches	216; Conservative 49; Mismatches 46; Indels 9; Gaps 3;			
RN	[3]			
RESULT 8				
Q6INT4		PRELIMINARY;	PRT;	311 AA.
ID	Q6INT4			
AC	Q6INT4;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DR	MGC80304 protein.			
GN	Name=MGC80304;			
OS	Xenopus laevis (African clawed frog)			
OC	Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Xenopodinae; Xenopus.			
NCBI_TAXID=8355;				
[1]	SEQUENCE FROM N.A.			
RC	TISSUE=Ovary;			
RX	Medline=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klaunier R.D., Collins F.S., Wagner L., Shevchenko C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko C., Prange C.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzyniak M.I., Skalska U., Smajlous D.B., Schnurch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human",			
RT	and mouse cDNA sequences", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RC	TISSUE=Ovary;			
RX	Medline=22341132; PubMed=12454917; DOI=10.1002/dudy.10174;			
RA	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,			
RA	Richardson P.; "Genetic and genomic tools for Xenopus research: The NIH Xenopus Initiative"; Dev. Dyn. 225:384-391(2002).			
RN	[3]			

RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC072178; AAH72178.1; -
 DR Interpro; IPR004046; GST_Cterm.
 DR Pfam; PF00043; GST_C; 1.
 SQ SEQUENCE 311 AA; 34424 MW; D5E8325C18D88751 CRC64;

Query Match 69.3%; Score 1146.5; DB 2; Length 311;
 Best Local Similarity 68.1%; Pred. No. 2..6e-86; Indels 9; Gaps 3;
 Matches 218; Conservative 44; Mismatches 49; Indels 9; Gaps 3;

Qy 1 MPWYKQPKYHGSAPRLVEPLCTMRLPNHTSKITSPATDAGHVOETSEPSIQALESRQD 60
 Db 1 MPWYKQPKYHGSAPRLVEPLCTMRLPNHTSKITSPATDAGHVOETSEPSIQALESRQD 52

Qy 61 DILKRYELKAADVGLSKMHTPDADLVNLIQADEPTLATMLDLSVLSKGDKYGAALK 120
 Db 53 DILKRYELKAADVGLSKMHTPDADLVNLIQADEPTLATMLDLSVLSKGDKYGAALK 112

Qy 121 DIVINANPASPPLSLVHLICERYLVRULSTVTHSSVKNVPENLKFGEOARKSRRHE 180
 Db 113 DIVINANPASPPLSLVHLICERYLVRULSTVTHSSVKNVPENLKFGEOARKSRRHE 172

Qy 181 YOLGFTLIVNKVQPKOMKSVQTMPIEGEYGNARFLSIFGOKHNAVTTLIDSWDIA 240
 Db 173 YOLGFTLIVNKVQPKOMKSVQTMPIEGEYGNARFLSIFGOKHNAVTTLIDSWDIA 232

Qy 241 MFOLREGSSKEKAIVFRSMNSALGRSPMWVGNELTADVVIWSVLQQTGGSSAAPTNVQ 300
 Db 233 IFOLRDGSSKEKAIVLAKMNTLGKSPWLVGNELTADVIVSWCAVQOCGNST-AVPNVQ 291

Qy 301 RWLKSCENLAPFSTALQLIK 320
 Db 292 KWWKSCENLASFKVRLK 311

RESULT 9

ID Q7ZYD7 PRELIMINARY; PRT; 311 AA.
 AC DT 01-JUN-2003 (TREMBREL_24, Created)
 DT 01-JUN-2003 (TREMBREL_24, Last sequence update)
 DE Jevi-prov protein.
 OS Xenopus laevis (African clawed frog).
 OC Amphibia; Batrachia; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Xeropoda; Xenopus.
 OC Xenopidae; Xenopus.
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shevchenko C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Blakesley R.W., Usdin T.B., Yoshiaki S., Carninci P., Prange C.,
 RA Rahm S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,
 RA Bosak S.A., Mcowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Farley J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalius D.E., Schnurch A., Schein J.E.,
 RA Jones S.J., Marra M.A.; NCBI_Taxid=8355;

RESULT 10

ID Q7T3C0 PRELIMINARY; PRT; 321 AA.
 AC DT 01-OCT-2003 (TREMBREL_25, Created)
 DT 01-OCT-2003 (TREMBREL_25, Last sequence update)
 DE ZGC:63976.
 GN OS ORFnames-ZGC:63976;
 OS Brachydanio rerio; (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophys; Cypriniformes;
 OC Cyprinidae; Danio.
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shevchenko C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Blatchenko L., Matsubara K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Cadavid T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Kara S.S., Logueillo N.A.M., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Boksa S.A., McBewan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzy D.N., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahay J., Heitman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalius D.E., Schnurch A., Schein J.B.,
 RA Jones S.J., Marras M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RR Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Kidney.
 RA Strausberg R.;
 RA Submitted (JUN-2003) to the EMBL/GenBank/DDBJ database.
 DR EMBL: BC053178; AAM53189; 1; -.
 DR ZFB-GENB-040426-zgc:63976.
 DR InterPro: IPR04046; GST_Cterm.
 DR InterPro: IPR010987; GST_C_like.
 PFam: PF00043; GST_C; 1
 DR SEQUENCE 321 AA; 34852 MW; BAB6B951208244A CRC64;
 Query Match 56.0%; Score 926.5; DB 2; Length 321;
 Best Local Similarity 57.3%; Pred. No. 4.1e-68;
 Matches 188; Conservative 48; Mismatches 77; Indels 15; Gaps 7;
 DR 1 MPWQVQKPHGGSAPLRVEPTCMWRLPNHHSKTS--PATDAGHVOETSEPSIQALES 57
 1 MPWQVKPV--SPADITVDPCTMVKLPNTHAQGASLGERALQNQEV---DPTKALEE 54
 DR 58 RQDILRKLYELKAADVGLSKMHTHPDADEPDVNT---LQADEPTTLATNTIDNSVLGK 114
 DR 55 RQDILRKLYELKAADVGLAKTVTTPDADEPDASTIAHTLHTHPDAVLRGTDADDLGK 114
 DR 115 DYGAIKDTIVNANPASPPLSLVHLRLLCERYRVSTVHHSVNVNPEMLVKCG-EQA 173
 DR 115 DSGAIRDIVINANPAPQPLSLLVHLRLLCERYRVSTVHHSVNVNPEMLVKCG-EQA 173
 DR 174 RKQSRHEYQIGFTLWKNVKTQMFPSVQTMCPFEGEYGNARFLFSLFG-QKHNAVTTL 232
 DR :|||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 DR 175 HSYARHRFQLGFTLWKNQSKLQMESTQNMCPISGEYGNARFLFSLFG-QKHNAVTTL 234
 DR 233 IDSMWIDIANFOLRSGSSEKKEAVFESMNALGRSPWLVGELTVAVWVWLSVLTQTGSS 292
 DR 235 MDGWVDTALFOLAEKGSKERAVLRAALGGRSPWLLQGBFSLAVIVSACCVLQNGQTS 294
 DR 293 GAATTNVORLKLSEENLAPSTALQLLK 320
 DR :|||:|||:|||:|||:
 DR 295 -SAPPNVQRWLKSCQNLGYFSCVDPLLQ 321
 RESULT 11
 Q07A3 PRELIMINARY; PRT; 340 AA.
 ID Q07A3 PRELIMINARY; PRT; 301 AA.
 AC Q07A3;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE AGF5808 (Fragment);
 GN Name=AGC0554; ORFName=ENSANGG0000011827;
 OS Anopheles gambiae str. REST.
 OC Bokuyaota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 NCBI_TAXID=160454;
 RN SEQUENCE FROM N.A.
 RP MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5451.2185;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Adams P.G., Scherer S.E., Li P.W., Hoskins R.A., Gallo R.F.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gallo R.F.,
 RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blakej R.G., Champe M., Preiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Abgyani A.H., An H.J., Andreus-Pfankoch C., Baldwin D.,
 RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brottner P.,
 RA Burtis K.C., Buzan D.A., Butler H., Cadieu E., Centen A., Chandra I.,
 RA Cherry J.M., Cowley S., Dahake C., Davenport L.B., Davies P.,
 RA De Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin R.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glaser K.,
 RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Sequencing from N.A.

QY 168 CFGGEQARKQSRRHRYQGFTLWIKNVPTQKRSVQTMCPISCEGNARFLSLFGOKNA 227 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 Db 171 VPVNPALP-----KISVTLWIKNCETEMSSPTMVPIGEVNTIYGRGVPAEYR 224 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 AC Q6NK04; 06NK04; PRELIMINARY; PRT; 322 AA.
 AC 06NK04; 06NK04; 2004 (T-EMBL; rel. 27, Created)
 DT 05-JUL-2004 (T-EMBL; rel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBL; rel. 27, Last annotation update)
 DE LP12149 (Fragment)
 OS Drosophila melanogaster (Fruit fly).
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydioidea; Drosophilidae; Drosophila;
 OC NCBI_TaxID:7227;
 DB 285 L 285 RN [1]
 DB 285 L 285 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.I.G.,
 RA Abril J.F., Agayani A.R., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Balow R.M., Beau A., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bobshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Botchan M.R., Butler H., Cadile E., Centner A., Chandra I.,
 RA Cherry J.M., Clewley S., Dahake C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Douc L.E., Downes M., Dragan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin R.K., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Habermann P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Klein M.-H., Ibegwam C.,
 RA Jalali M., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Kelchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mlsihina N.V., Mobarry C., Morris J., Mosherfi A.,
 RA Mount S.M., Moy M., Murphy L., Muany D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nussekern D.R., Pacieb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Sider-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
 RA Svirska R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP GENOME REANNOTATION.
 RX MEDLINE=2242609; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Wilhelmi E.J., Bayraktaroglu L., Bernat B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.";
 RT Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
 RL "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.";
 RT Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
 CC -1- FUNCTION: Probable core protein of the multisyntetase complex
 CC that serves as a template for the assembly of the supramolecular
 CC structure (By similarity).
 CC -1- SUBUNIT: Component of the multisyntetase complex which is
 CC comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, the
 CC monospecific isoleucyl-leucyl-glutaminyl-methionyl-lysyl
 CC arginyl-, and aspartyl-tRNA synthetases as well as three auxiliary
 CC proteins, p18, p48 and p43 (By similarity).
 CC -1- SIMILARITY: Contains 1 GSP-like domain.

RESULT 15
 MCA2_DROME STANDARD; PRT; 334 AA.
 ID MCA2_DROME
 AC Q9VUR3;
 DT 16-OCT-2001 (Rel. 40, Created)

Search completed: February 23, 2005, 13:57:15
Job time : 61.9811 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 23, 2005, 13:25:39 ; Search time 102.258 Seconds

1758.725 Million cell updates/sec

Title: US-10-622-817-8
Perfect score: 2596
Sequence: I MIVFVRENSSHGFPPVEVD... CWNNGCBWNRVCMKDHHFEDV 465

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Genesed_16pec04:
1: geneseqP1980b: *
2: geneseqP1990b: *
3: geneseqP2000b: *
4: geneseqP2001b: *
5: geneseqP2002b: *
6: geneseqP2003ab: *
7: geneseqP2003bs: *
8: geneseqP2004b: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2596	100.0	465	2	AAY32501 Aay32501 Human par
2	2596	100.0	465	6	AAB30800 Abo07156 Human par
3	2596	100.0	465	6	AAB30801 Aay32502 Human par
4	2584	99.5	465	6	AAB30801 Aay32502 Human par
5	2405	92.6	437	2	AAY32502 Abo07157 Human p53
6	2405	92.6	437	6	AAB67517 Amino acid Aab67531 Amino acid
7	2170.5	83.6	464	4	AAB67517 Aab67531 Amino acid
8	2165.5	83.4	464	4	AAB67531 Aab67532 Amino acid
9	2165.5	83.4	464	4	AAB67531 Aab67533 Amino acid
10	2087.5	80.4	451	4	AAB67533 Abo07158 Human p53
11	1696.5	65.4	316	6	AAB67533 Abo07158 Human p53
12	1696.5	64.7	344	4	AAB67531 Amino acid Aab67517 Amino acid
13	1234.5	47.6	296	4	AAB67526 Amino acid Aab67522 Amino acid
14	1058.5	40.8	468	4	AAB65114 Amino acid Aab67523 Amino acid
15	1002	38.6	250	4	AAB67519 Amino acid Aab67519 Amino acid
16	997	38.4	262	4	AAB67518 Amino acid Aab67518 Amino acid
17	870	33.5	156	4	AAG67213 Amino acid Aab67521 Amino acid
18	671.5	25.9	183	4	AAB67525 Amino acid Aab67524 Amino acid
19	671.5	25.9	194	4	AAB67524 Aab686951 C. elegan
20	544.5	21.0	386	4	AAB686951 Aab67523 Amino acid
21	506	19.5	153	4	AAB67523 pab67529 Amino acid
22	335	12.9	77	4	AAB67529 ham1055 Peptide #
23	263	10.1	46	4	AAM17055 Peptide # AbB36052
24	263	10.1	46	4	AAM29548 Peptide # ham29548
25	263	10.1	46	4	AAM29548 Peptide # ham29548

Minimum DB seq length: 0

Maximum DB seq length: 200000000

ALIGNMENTS

25	263	10.1	46	4	ABB30873 AAB21452 Protein #
27	263	10.1	46	4	AAM69222 Human bon
28	263	10.1	46	4	AAM56339 Human bra
29	263	10.1	46	4	ABG5098 Human liv
30	263	10.1	46	4	ABG38830 Human pep
31	263	10.1	46	5	ABG38830 Human pep
32	252	9.7	106	8	ADM96899 Modified
33	251	9.7	63	4	AAB67522 Amino aci
34	251	9.7	105	4	AAB67520 Amino aci
35	251	9.7	105	8	ADM96487 Modified
36	240.5	9.3	503	4	ABB61708 Drosophil
37	240	9.3	503	7	AAB67082 Ariadne-1
38	240	9.2	511	4	Abb63665 Drosophil
39	239	9.2	520	8	AAB22562 Sea-squir
40	236.5	9.1	445	3	Aab21034 Human nuc
41	236.5	9.1	445	8	Adq96154 T cell ac
42	236.5	9.1	445	8	Adq96026 T cell ac
43	236.5	9.1	557	3	Ray98059 Human Rin
44	236.5	9.1	557	8	Adq96028 T cell ac
45	236	9.1	53	4	Aab67528 Amino aci

RESULT 1
AYY32501
ID AYY32501 standard; protein; 465 AA.
XX
AC AYY32501;
XX
DT 21-OCT-1999 (first entry)
DE Human parkin gene variant protein.
XX
KW Parkinson's disease related gene; parkin gene; variant; gene therapy.
XX
OS Homo sapiens.
XX
PN WO9940191-A1.
XX
PR 09-FEB-1999; 99WO-JP000545.
PR 09-FEB-1999; 98JP-00027531.
PA (SHIMIZU) SHIMIZU N.
PA (MIZU) MIZUNO Y.
XX
PI Shimizu N, Mizuno Y;
XX
DR WPI; 1999-494295/41.
DR -PSDB; AAX99923.
XX
PT Gene implicated in the pathology of Parkinson's disease, used for treatment of the disease.
XX
PS Claim 1; Page 83-88; 114PP; English.
XX
CC This sequence is encoded by a gene of the invention, and is implicated in the pathology of Parkinson's disease. This sequence is a variant of the gene found in parkinson's disease patients. The sequences may be used for the diagnosis, treatment (including gene therapy) and investigation of Parkinson's disease

SQ Sequence 465 AA;

Query Match 100.0%; Score 2596; DB 2; Length 465;
Best Local Similarity 100.0%; Pred. No. 2.3e-219;
Matches 465; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MIVFVRENSSHGFPPVEVDSDTSIFQLKEVAKRQGVPAQDQLRVIFAGKELRNDDWTVQNCD 60

Db 1 ||||||| 60
 QY 61 LDQOSIYHIVORPKQEMMAGTGGDPRNAAAGCERBPPSITRVDLSSVLPGSVGLA 120
 Db 61 LDQOSIYHIVORPKQEMMAGTGGDPRNAAAGCERBPPSITRVDLSSVLPGSVGLA 120
 QY 121 VILHTDSRKDSPAGSPAGRSIINSFYVICKGCPQRVQPGKLRVOCSTCRQATLTQGP 180
 Db 121 VILHTDSRKDSPAGSPAGRSIINSFYVICKGCPQRVQPGKLRVOCSTCRQATLTQGP 180
 QY 181 SCWDDVLINPMSGEQSPHCPGTSAFFFGGAHTSDKETPVVALHILATNSRNCIT 240
 Db 181 SCWDDVLINPMSGEQSPHCPGTSAFFFGGAHTSDKETPVVALHILATNSRNCIT 240
 QY 241 CTDVRSPLVQCNRSRHTIDCFHLYCVTRNLNDQFVDPQGSLPCVAGCNSLIKE 300
 Db 241 CTDVRSPLVQCNRSRHTIDCFHLYCVTRNLNDQFVDPQGSLPCVAGCNSLIKE 300
 QY 301 LHFRIGEBCQNYQQYGAECVCLQMGVLCPRGCGAGLILPSPDORKTCCEGGNGLC 360
 Db 301 LHFRIGEBCQNYQQYGAECVCLQMGVLCPRGCGAGLILPSPDORKTCCEGGNGLC 360
 AC AA330800;
 XX DT 24-FEB-2003 (first entry)
 DE Human Parkin protein.
 XX Human; Parkin protein; neurological disorder; apoptosis; gene therapy;
 KW ischaemic stroke; Parkinson's disease; Alzheimer's disease; nootropic;
 KW transgenic; cerebroprotective; neuroprotective; neurotransplantation.
 OS Homo sapiens.
 FH Key Location/qualifiers
 FT Cleavage-site 126
 PN WO200279459-A2.
 PD 10-OCT-2002.
 XX 02-APR-2002; 2002WO-DK000221.
 PR 29-MAR-2001; 2001DK-00000525.
 PR 03-APR-2001; 2001US-0281286P.
 PA (NSGE-) NSGENE AS.
 XX Jensen PH;
 PT XX
 DR 13-AUG-2003 (first entry)
 N-PSDB; AAD4679.
 XX New isolated nucleic acid sequence encoding a Parkin polypeptide, useful
 PT for treating, preventing or diagnosing neurological disorders, e.g.
 PT Parkinson's disease, Alzheimer's disease or ischemic stroke, and in
 PT screening assays.
 PS Claim 10; Page 69; 71pp; English.

RESULT 2
 AAE30800
 ID AAE30800 standard; protein; 465 AA.
 XX AC AA330800;
 XX DT 24-FEB-2003 (first entry)
 DE Human Parkin protein.
 XX Human; Parkin protein; neurological disorder; apoptosis; gene therapy;
 KW ischaemic stroke; Parkinson's disease; Alzheimer's disease; nootropic;
 KW transgenic; cerebroprotective; neuroprotective; neurotransplantation.
 OS Homo sapiens.
 FH Key Location/qualifiers
 FT Cleavage-site 126
 PN WO200279459-A2.
 PD 10-OCT-2002.
 XX 02-APR-2002; 2002WO-DK000221.
 PR 29-MAR-2001; 2001DK-00000525.
 PR 03-APR-2001; 2001US-0281286P.
 PA (NSGE-) NSGENE AS.
 XX Jensen PH;
 PT XX
 DR 13-AUG-2003 (first entry)
 N-PSDB; AAD4679.
 XX New isolated nucleic acid sequence encoding a Parkin polypeptide, useful
 PT for treating, preventing or diagnosing neurological disorders, e.g.
 PT Parkinson's disease, Alzheimer's disease or ischemic stroke, and in
 PT screening assays.
 PS Claim 10; Page 69; 71pp; English.

RESULT 3
 ABO07156
 ID ABO07156 standard; protein; 465 AA.
 XX AC ABO07156;
 XX DT 13-AUG-2003 (first entry)
 DE Human p53 modifying protein, SEQ ID 116.
 XX Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;
 KW antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;
 KW lung cancer; ovarian cancer; angiogenesis; cell cycle;
 KW apoptotic disorder; cell proliferation disorder.
 OS Homo sapiens.

XX
 CC The invention relates to Parkin protein and its corresponding nucleic
 CC acid sequence. The nucleic acid sequence is useful for altering the
 proteolytic processing of Parkin at its potential cleavage site at Asp
 126. The invention is used in manufacturing or testing a pharmaceutical
 composition for treating and/or preventing a neurological disorder, e.g.
 Alzheimer's disease or ischaemic stroke. It also used for detecting the
 occurrence of proteolytic processing of Parkin at Asp 126 in a sample, in
 monitoring a potential disposition for a neurodegenerative disease, and
 for treating, preventing and/or diagnosing Parkinson's disease or other
 neurodegenerative disorders. The viral vector is used for transforming
 neuronal cells in vivo or ex vivo. The invention is useful for
 neurotransplantation into the CNS of a mammal. It may be used in
 screening assays to identify compounds that increase or decrease
 apoptosis. It is also used in gene therapy. The present sequence is human
 Parkin protein.

XX Sequence 465 AA;
 Query Match 100.0%; Score 2596; DB 6; Length 465;
 Best Local Similarity 100.0%; Pred. No. 2,3e-219; Matches 465; Mismatches 0; Indels 0; Gaps 0;
 Matches 465; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIVFVERNSHSGFPVIEUDTSIRDLKAVRQVPAQDQLRVFAGELRNWTVQND
 Db 1 MIVFVERNSHSGFPVIEUDTSIRDLKAVRQVPAQDQLRVFAGELRNWTVQND
 QY 61 LDQOSIYHIVORPKQEMMAGTGGDPRNAAAGCERBPPSITRVDLSSVLPGSVGLA 120
 Db 1 LDQOSIYHIVORPKQEMMAGTGGDPRNAAAGCERBPPSITRVDLSSVLPGSVGLA 120
 QY 61 SCWDDVLINPMSGEQSPHCPGTSAFFFGGAHTSDKETPVVALHILATNSRNCIT 240
 Db 61 SCWDDVLINPMSGEQSPHCPGTSAFFFGGAHTSDKETPVVALHILATNSRNCIT 240
 QY 121 VILHTDSRKDSPAGSPAGRSIINSFYVICKGCPQRVQPGKLRVOCSTCRQATLTQGP 180
 Db 121 VILHTDSRKDSPAGSPAGRSIINSFYVICKGCPQRVQPGKLRVOCSTCRQATLTQGP 180
 QY 181 SCWDDVLINPMSGEQSPHCPGTSAFFFGGAHTSDKETPVVALHILATNSRNCIT 240
 Db 181 SCWDDVLINPMSGEQSPHCPGTSAFFFGGAHTSDKETPVVALHILATNSRNCIT 240
 QY 241 CTDVRSPLVQCNRSRHTIDCFHLYCVTRNLNDQFVDPQGSLPCVAGCNSLIKE 300
 Db 241 CTDVRSPLVQCNRSRHTIDCFHLYCVTRNLNDQFVDPQGSLPCVAGCNSLIKE 300
 QY 301 LHFRIGEBCQNYQQYGAECVCLQMGVLCPRGCGAGLILPSPDORKTCCEGGNGLC 360
 Db 301 LHFRIGEBCQNYQQYGAECVCLQMGVLCPRGCGAGLILPSPDORKTCCEGGNGLC 360
 QY 361 GFAFCRECKEAYHEGCSAVFASGTITQAYVDERAERQWEAKSETIKTTKPCPR 420
 Db 361 GFAFCRECKEAYHEGCSAVFASGTITQAYVDERAERQWEAKSETIKTTKPCPR 420
 QY 421 CHYVERKNGGMKMCQPOQCRLEWCWNCGEGEWNRVCMGDHWFDV 465
 Db 421 CHYVERKNGGMKMCQPOQCRLEWCWNCGEGEWNRVCMGDHWFDV 465

PN WO200299122-A1.
 XX
 PD 12-DEC-2002.
 XX
 PP 03-JUN-2002; 2002WO-US017382.
 PR 05-JUN-2001; 2001US-0296076P.
 PR 10-OCT-2001; 2001US-0328605P.
 PR 15-FEB-2002; 2002US-0357203P.
 XX
 PA (EXEL-) EXELIXIS INC.
 PI Friedman L, Plouman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
 XX WPI; 2003-156859/15.
 DR N-PSDB; ACD1332.
 XX
 PT Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53 pathway in *Drosophila*.
 XX
 PS Example 2; Page 399-401; 678pp; English.
 XX
 CC The invention relates to identifying (M1) a candidate p53 pathway modulating agent, by contacting an assay system comprising a purified HM polypeptide (human orthologue of genes that modify the p53 pathway in *Drosophila*) or nucleic acid with a test agent under conditions, where but for the presence of the test agent, the system provides a reference activity, and detecting a test agent-biased activity of the assay system.
 CC Also included are modulating (N12) a p53 pathway of a cell (comprising contacting a cell defective in p53 function with a candidate modulator that specifically binds to a HM polypeptide comprising an HM amino acid sequence, where p53 function is restored), modulating (N3) a p53 pathway in a mammalian cell (comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with a probe for HM expression; (c) comparing the results with a control; and (d) determining whether the comparison indicates a likelihood disease). (M1) is useful for identifying modulators of the p53 pathway. A probe for HM expression is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 % expression level. Modulators identified by (M1) are useful in a variety of diagnostic and therapeutic applications, where disease or disorder prognosis is related to defects in the p53 pathway, such as, angiogenesis, apoptosis or cell proliferation disorders (e.g. cancer). Another two new methods (M2 and M3) are useful for modulating the p53 pathway of a cell, thus restoring the p53 function of the cell, so that the cell undergoes normal proliferation or progression through the cell cycle. (M2) and (M3) are also useful for treating defects in the p53 pathway such as angiogenic, apopotic or cell proliferation disorders. The present sequence (CC) represents a human p53 pathway modifying protein
 XX
 SQ sequence 465 AA;

Query Match 100.0%; Score 2596; DB 6; Length 465;
 Best Local Similarity 100.0%; Pred. No. 2.3e-219;
 Matches 465; Conservative 0; Mismatched 0; Indels 0; Gaps 0;

Qy 1 MIVFVRFNSHGFPPVEVDSPSIFOLKEVAKRQGPADQLVIRAGKEURNDWTQNC 60
 1 MIVFVRFNSHGFPPVEVDSPSIFOLKEVAKRQGPADQLVIRAGKEURNDWTQNC 60
 Qy 61 LDQGSTIWHIVQRPWPKQEMMNATGGDPRNAAAGGCEERPOSTIVDVLSSSLPGDSVGLA 120
 61 LDQGSTIWHIVQRPWPKQEMMNATGGDPRNAAAGGCEERPOSTIVDVLSSSLPGDSVGLA 120
 XX
 PI Jensen PH;
 XX
 DR WPI; 2003-046812/04.
 DR N-PSDB; AAD47680.

XX
 PT New isolated nucleic acid sequence encoding a Parkin polypeptide, useful for treating, preventing or diagnosing neurological disorders, e.g. Parkinson's disease, Alzheimer's disease or ischemic stroke, and in screening assays.
 XX
 PS Claim 10; Page 71; 71pp; English.

XX
 CC The invention relates to Parkin protein and its corresponding nucleic acid sequence. The nucleic acid sequence is useful for altering the proteolytic processing of Parkin at its potential cleavage site at Asp 126. The invention is used in manufacturing or testing a pharmaceutical composition for treating and/or preventing a neurological disorder, e.g.

CC 181 SCWDDVLIIPNRMSGECPSPHCPTSAFFFKCGAHPISDKEPVALTHIATNSRNITCIT 240
 241 CTDVRSPLVFCSNSRIVTCICDFHIVCYTRINDRDPHDPOLGSPCPVCAGCPNSLKE 300
 241 CTDVRSPLVFCSNSRIVTCICDFHIVCYTRINDRDPHDPOLGSPCPVCAGCPNSLKE 300
 DB 301 LHFRIGEQQNYQOYGAECVLOQNGVLCPRPGGAGLLEPEPDORKVTCEGGNGGC 360
 301 LHFRIGEQQNYQOYGAECVLOQNGVLCPRPGGAGLLEPEPDORKVTCEGGNGGC 360
 Qy 361 GFACRCRCKEAYHEGCSAVFFASGT"TAQYRVDERAEQARWEASKETIKTTKPPR 420
 DB 361 GFACRCRCKEAYHEGCSAVFFASGT"TAQYRVDERAEQARWEASKETIKTTKPPR 420
 Qy 421 CHVPEVNGGCHMKPQPQRLEWCWNCWNGCENWRVGMGDWFDV 465
 DB 421 CHVPEVNGGCHMKPQPQRLEWCWNCWNGCENWRVGMGDWFDV 465

RESULT 4
 AAE30801
 ID AAE30801 standard; protein; 465 AA.
 XX
 AC AAE30801;
 XX
 DT 24-FEB-2003 (first entry)
 XX
 DE Human Parkin D126 mutant protein.
 KW Human; Parkin protein; neurological disorder; apoptosis; gene therapy; ischemic stroke; Parkinson's disease; Alzheimer's disease; nootropic; transgenic; cerebroprotective; neuroprotective; neurotransplantation; mutant; murein.
 XX
 OS Homo sapiens.
 XX
 FH Synthetic.
 FT Key Location/Qualifiers
 FT Misc-difference 126 /note= "Wild-type Asp is replaced with Glu"
 FT Cleavage-site 126 /note= "Encoded by CCA"
 FT Misc-difference 223 /note= "Encoded by CCA"
 XX
 PN WO200279459-A2.
 XX
 PD 10-OCT-2002.
 XX
 PP 02-APR-2002; 2002WO-DK000221.
 XX
 PR 29-MAR-2001; 2001DK-0000525.
 PR 03-APR-2001; 2001US-0281286P.
 XX
 PA (NSGE-) NSGENE AS.
 XX
 PI Jensen PH;
 XX
 DR WPI; 2003-046812/04.
 DR N-PSDB; AAD47680.

XX
 PT New isolated nucleic acid sequence encoding a Parkin polypeptide, useful for treating, preventing or diagnosing neurological disorders, e.g. Parkinson's disease, Alzheimer's disease or ischemic stroke, and in screening assays.
 XX
 PS Claim 10; Page 71; 71pp; English.

XX
 CC The invention relates to Parkin protein and its corresponding nucleic acid sequence. The nucleic acid sequence is useful for altering the proteolytic processing of Parkin at its potential cleavage site at Asp 126. The invention is used in manufacturing or testing a pharmaceutical composition for treating and/or preventing a neurological disorder, e.g.

CC 181 SCWDDVLIIPNRMSGECPSPHCPTSAFFFKCGAHPISDKEPVALTHIATNSRNITCIT 240

CC Alzheimer's disease or ischaemic stroke. It also used for detecting the occurrence of proteolytic processing of Parkin at Asp 126 in a sample, in monitoring a potential disposition for a neurodegenerative disease, and for treating, preventing and/or diagnosing Parkinson's disease or other neurodegenerative disorders. The viral vector is used for transforming neuronal cells in vivo or ex vivo. The invention is useful for neurotransplantation into the CNS of a mammal. It may be used in screening assays to identify compounds that increase or decrease apoptosis. It is also used in gene therapy. The present sequence is human
 CC Parkin mutant protein
 XX SQ Sequence 465 AA;

Query Match 99.5%; Score 2584; DB 6; Length 465;
 Best Local Similarity 99.6%; Pred. No. 2.6e-218; Matches 463; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 CC QY 1 MIVFVRPNSSHGFPPVEDSDTSIROLKEVAKRQGVPAQDQLRVIFAGKELRNDWTVQCD 60
 DB 1 LDQOSIVHIVQRPKQGQMANATGGDPDPRNAAGGEREQSLTRVDLSSSVLPGSVGLA 60
 QY 61 LDQOSIVHIVQRPKQGQMANATGGDPDPRNAAGGEREQSLTRVDLSSSVLPGSVGLA 60
 DB 61 LDQOSIVHIVQRPKQGQMANATGGDPDPRNAAGGEREQSLTRVDLSSSVLPGSVGLA 120
 QY 121 VILHDTSRKDSPPAGSPARSINSYVYCKGKCORVPGKLCVQSCSTCRQALITLTQGP 180
 DB 121 VILHDTSRKDSPPAGSPARSINSYVYCKGKCORVPGKLCVQSCSTCRQALITLTQGP 180
 QY 181 SCWDVDLIPNRMSB3COSHCPGSAEFFFKGAHPSTDKEPVHLIAATNSRNCT 240
 DB 181 SCWDVDLIPNRMSB3COSHCPGSAEFFFKGAHPSTDKEPVHLIAATNSRNCT 240
 QY 241 CTDVRSPVLFQCNRSRHLVCLDFPHLYCVTRLANDRQFVHDPOLGYSLPCVAGCPNSLIKE 300
 DB 241 CTDVRSPVLFQCNRSRHLVCLDFPHLYCVTRLANDRQFVHDPOLGYSLPCVAGCPNSLIKE 300
 QY 301 LHFRILGEQEQQNYQQYGAECVULQMGVLPRPGCGAGLLEPFDORKVTCEGGNGLC 360
 DB 301 LHFRILGEQEQQNYQQYGAECVULQMGVLPRPGCGAGLLEPFDORKVTCEGGNGLC 360
 QY 361 GFAFCRECKEAYHEGECSAVFEEASGTTOQAYRUDERAEAOARWEASKETTKTTPCPR 420
 DB 361 GFAFCRECKEAYHEGECSAVFEEASGTTOQAYRUDERAEAOARWEASKETTKTTPCPR 420
 QY 421 CHVVEKNGGCHMMKCPQPCRLECWNCNGCEWMRVCMGDHWFDV 465
 DB 421 CHVVEKNGGCHMMKCPQPCRLECWNCNGCEWMRVCMGDHWFDV 465
 RESULT 5
 AAY3202 ID AAY32502 standard; protein; 437 AA.
 AC AAY32502;
 XX DT 21-OCT-1999 (first entry)
 DE Human parkin gene variant protein.
 XX
 KW Parkinson's disease related gene; parkin gene; variant; gene therapy.
 XX OS Homo sapiens.
 XX PN W09940191-A1.
 XX PD 12-AUG-1999.
 XX PF 09-FEB-1999; 99WO-JP000545.
 XX PR 09-FEB-1998; 98JP-00027531.
 PA (SHIMIZU N.

PA (MIZU/) MIZUNO Y.
 XX Shimizu N, Mizuno Y;
 PT XX
 DR N-PSDB; AAX9924.
 XX Gene implicated in the pathology of Parkinson's disease, used for treatment of the disease.
 XX RS Claim 1; Page 89-94; 114PP; English.
 XX This sequence is encoded by a gene of the invention, and is implicated in the pathology of Parkinson's disease. This sequence is a variant of the parkin gene found in parkinson's disease patients. The sequences may be used for the diagnosis, treatment (including gene therapy) and investigation of Parkinson's disease
 XX SQ Sequence 437 AA;

Query Match 92.6%; Score 2495; DB 2; Length 437;
 Best Local Similarity 94.0%; Pred. No. 1.3e-202; Matches 437; Conservative 0; Mismatches 0; Indels 28; Gaps 1;
 CC QY 1 MIVFVRPNSSHGFPPVEDSDTSIROLKEVAKRQGVPAQDQLRVIFAGKELRNDWTVQCD 60
 DB 1 MIVFVRPNSSHGFPPVEDSDTSIROLKEVAKRQGVPAQDQLRVIFAGKELRNDWTVQCD 60
 QY 61 LDQOSIVHIVQRPKQGQMANATGGDPDPRNAAGGEREQSLTRVDLSSSVLPGSVGLA 120
 DB 61 LDQOSIVHIVQRPKQGQMANATGGDPDPRNAAGGEREQSLTRVDLSSSVLPGSVGLA 120
 QY 121 VILHDTSRKDSPPAGSPARSINSYVYCKGKCORVPGKLCVQSCSTCRQALITLTQGP 240
 DB 121 VILHDTSRKDSPPAGSPARSINSYVYCKGKCORVPGKLCVQSCSTCRQALITLTQGP 240
 QY 181 SCWDVDLIPNRMSB3COSHCPGSAEFFFKGAHPSTDKEPVHLIAATNSRNCT 300
 DB 181 SCWDVDLIPNRMSB3COSHCPGSAEFFFKGAHPSTDKEPVHLIAATNSRNCT 300
 QY 241 CTDVRSPVLFQCNRSRHLVCLDFPHLYCVTRLANDRQFVHDPOLGYSLPCVAGCPNSLIKE 360
 DB 241 CTDVRSPVLFQCNRSRHLVCLDFPHLYCVTRLANDRQFVHDPOLGYSLPCVAGCPNSLIKE 360
 QY 301 LHFRILGEQEQQNYQQYGAECVULQMGVLPRPGCGAGLLEPFDORKVTCEGGNGLC 420
 DB 301 LHFRILGEQEQQNYQQYGAECVULQMGVLPRPGCGAGLLEPFDORKVTCEGGNGLC 420
 QY 361 GFAFCRECKEAYHEGECSAVFEEASGTTOQAYRUDERAEAOARWEASKETTKTTPCPR 465
 DB 361 GFAFCRECKEAYHEGECSAVFEEASGTTOQAYRUDERAEAOARWEASKETTKTTPCPR 465
 QY 421 CHVVEKNGGCHMMKCPQPCRLECWNCNGCEWMRVCMGDHWFDV 437
 DB 421 CHVVEKNGGCHMMKCPQPCRLECWNCNGCEWMRVCMGDHWFDV 437
 RESULT 6
 ABO07157 ID ABO07157 standard; protein; 437 AA.
 AC ABO07157;
 XX DT 13-AUG-2003 (first entry)
 DE Human p53 modifying protein, SEQ ID 117.
 XX
 KW Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;
 KW antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;
 KW lung cancer; ovarian cancer; angiogenesis; cell cycle;
 KW apoptotic disorder; cell proliferation disorder.
 XX OS Homo sapiens.

XX	181 SCDDWLLPNMNSGECQSPHPGTSLEFFFCGAHSTSKEPTPVHLIAINSRNITCT 240	Qy	
PN	WO200299122-A1.	Db	179 -----EFFKCGAHTSDKTPVHLIAINSRNITCT 212
XX		Db	12-DEC-2002.
PD		Qy	03-JUN-2002; 2002WO-US017382.
XX		PR	05-JUN-2001; 2001US-0296076P.
		PR	10-OCT-2001; 2001US-03280505P.
		PR	15-FEB-2002; 2002US-0357253P.
XX		PA	(EXEL-) EXELIXIS INC.
XX	Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53 pathway in <i>Drosophila</i> .	PT	N-P5DB; ACD13333.
XX		PT	Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53 pathway in <i>Drosophila</i> .
PS	Example 2, Page 401-402; 678pp; English.	PT	WPI; 2003-15689/15.
XX	The invention relates to identifying (M1) a candidate p53 pathway modulating agent, by contacting an assay system comprising a purified HM polypeptide (human orthologue of genes that modify the p53 pathway in <i>Drosophila</i>) or nucleic acid with a test agent under conditions, where but for the presence of the test agent, the system provides a reference activity, and detecting a test agent-biased activity of the assay system. Also included are modulating (M2) a p53 pathway of a cell (comprising contacting a cell defective in p53 function with a candidate modulator that specifically binds to a HM polypeptide comprising an HM amino acid sequence, where p53 function is restored), modulating (M3) a p53 pathway in a mammalian cell (comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with a probe for HM expression; (c) comparing the results with a control; and (d) determining whether the comparison indicates a likelihood disease). (M1) is useful for identifying modulators of the p53 pathway. A probe for HM expression is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 % expression level. Modulators identified by (M1) are useful in a variety of diagnostic and therapeutic applications, where disease or disorder prognosis is related to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell proliferation disorders (e.g. cancer). Another two new methods (M2 and M3) are useful for modulating the p53 pathway of a cell, thus restoring the p53 function of the cell, so that the cell undergoes normal proliferation or progression through the cell cycle. (M2) and (M3) are also useful for treating defects in the p53 pathway such as angiogenic, apoptotic or cell proliferation disorders. The present sequence represents a human p53 pathway modifying protein.	PT	DR
XX	Sequence 437 AA;	PT	N-P5DB; ACD13333.
Query	Match 92.6%; Score 2405; DB 6; Length 437;	SQ	
Best	Local Similarity 94.0%; Pred. No. 1; e-202;	PS	
Matches	437; Conservative 0; Mismatches 0; Indels 28; Gaps 1;	PS	
Qy	1 MIVFVRENSSAGFPVEVDSDTSIFOLKEVAKRQGHPADQIRVFAKELRNWTQNCD 60	CC	The present sequence represents a murine parkin2 polypeptide. Mutations or deletions in the parkin2 gene cause Parkinson's disease in humans. The
Db	1 MIVFVRENSSAGFPVEVDSDTSIFOLKEVAKRQGHPADQIRVFAKELRNWTQNCD 60	CC	human parkin2 gene is located in gene region 6q25.2-27. Parkin2 polypeptides and polynucleotides are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's
Qy	61 IQQQTHIVPWRKQEMNTTGGDPRNAAAGCEREPOSIITRVNLSSSVLPGDSVGLA 120	CC	disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, Multi-system atrophy, Wilson's disease, Pick's disease, Prion disease, and secondary causes inducing Parkinson's symptoms like toxins, drugs, brain tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated with a less active or non-active
Db	61 IQQQTHIVPWRKQEMNTTGGDPRNAAAGCEREPOSIITRVNLSSSVLPGDSVGLA 120	CC	parkin protein
Qy	121 VILHTSRKDSPAGSPAGSAGRSYNSPVYCKPCQRYQPKURQSTCROTQITQTGP 180	CC	
Qy	121 VILHTSRKDSPAGSPAGSAGRSYNSPVYCKPCQRYQPKURQSTCROTQITQTGP 180	CC	
Db	121 VILHTSRKDSPAGSPAGSAGRSYNSPVYCKPCQRYQPKURQSTCROTQITQTGP 178	CC	

SO	Sequence 464 AA;	PT	a transgenic non-human animal as an animal model for neurodegenerative diseases.
Query Match	83.6%; Score 2170.5; DB 4; Length 464;	PT	
Best Local Similarity	83.4%; Pred. No. 66-182;	XX	
Matches	388; Conservative 29; Mismatches 47; Indels 1; Gaps 1;	PS	Claim 7; Page 47-49; 62pp; English.
Qy	1 MIVFVRNSHGGPPVEVDTSIFOLKEVAKRQGPADQRVIFAGKEIRNDWTVQND	CC	The present sequence represents a murine parkin2 polypeptide. The sequence contains the mutation Lys161Arg. Mutations or deletions in the parkin2 gene cause Parkinson's disease in humans. The human parkin gene is located in gene region 6q25.2-27. Parkin2 polypeptides and polymucleorides are useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, Multi-system atrophy, Wilson's disease, Pick's disease, Prion disease, and secondary causes inducing Parkinson's syndromes like toxins, drugs, brain tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated with a less active or non-active parkin protein.
Db	1 MIVFVRNSHGGPPVEVDTSIFOLKEVAKRQGPADQRVIFAGKEIRNDWTVQND	CC	
Qy	61 LDQOSIVHIVPWRPKQGMNATGGDPRAAGGEREPOSLTRVDSLSSVLPDSVGLA	CC	
Db	61 LDQOSIVHIVPWRPKQGMNATGGDPRAAGGEREPOSLTRVDSLSSVLPDSVGLA	CC	
Qy	121 VILHDSRKRSSEAAKGPV-KPTYNSPFPYCKGPCHKVQGTCRQATLTLAQGP	CC	
Db	121 VILHDSRKRSSEAAKGPV-KPTYNSPFPYCKGPCHKVQGTCRQATLTLAQGP	CC	
Qy	181 SCWDDVLIPNRMSCGECQSPICPGTSAEFFFKCGAHPTSDKETPVALKHTATSRNITCIT	CC	
Db	180 SCWDDVLIPNRMSCGECQSPICPGTSAEFFFKCGAHPTSDKETPVALKHTATSRNITCIT	CC	
Qy	241 CTDVRSPVLFVQCNHRHVICLDFCHLYCVTRLNDROFVHDPOLGYSUPCVAQCPNSLIKE	CC	
Db	240 CTDVRSPVLFVQCNHRHVICLDFCHLYCVTRLNDROFVHDPOLGYSUPCVAQCPNSLIKE	CC	
Qy	301 LHHRFLIGEQQYNYQYQGAEBCVLQMGGLCPRPGCGAGLIPEDQPKVTEBGGNGLGC	360	
Db	300 LHHRFLIGEQQYNYQYQGAEBCVLQMGGLCPRPGCGAGLIPEDQPKVTEBGGNGLGC	359	
Qy	361 GFAFRCRECKEAVHNGECSAVFAASGTTQAVDRDAAEQAARWEAKSETIKKKTPCPR	420	
Db	360 GFVFRCRDCKEAVHNGCDPSLLEPSGATSQAVYRUDKRAAEQARWEAKSETIKKKTPCPR	419	
Qy	421 CHVVEKGNGCMMHKCPQPQCKLEWCMNGCEWNRVCMGDHWFDV	465	
Db	420 CHVVEKGNGCMMHKCPQPQCKLEWCMNGCEWNRVCMGDHWFDV	464	
RESULT 8		SO	Sequence 464 AA;
AAB67531		Query Match	83.4%; Score 2165.5; DB 4; Length 464;
ID AAB67531	standard; protein; 464 AA.	Best Local Similarity	83.2%; Pred. No. 1-78-181;
AC AAB67531;		Matches	29; Mismatches 48; Indels 1; Gaps 1;
XX DT 29-MAY-2001 (first entry)		Qy	1 MIVFVRNSHGGPPVEVDTSIFOLKEVAKRQGPADQRVIFAGKEIRNDWTVQND
DB DE Amino acid sequence of a mutated murine parkin2 polypeptide.		Db	1 MIVFVRNSHGGPPVEVDTSIFOLKEVAKRQGPADQRVIFAGKEIRNDWTVQND
XX KW Parkinson2; Parkinson's disease; 6q25.2-27; neurodegenerative disease; Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis; Multi-system atrophy; Wilson's disease; Pick's disease; Prion disease; brain tumour; head trauma; stroke; vascular irregularity; metabolic irregularity.		Qy	61 LDQOSIVHIVPWRPKQGMNATGGDPRAAGGEREPOSLTRVDSLSSVLPDSVGLA
OS Mus sp.		Db	61 LDQOSIVHIVPWRPKQGMNATGGDPRAAGGEREPOSLTRVDSLSSVLPDSVGLA
XX PN EP1081225-A1.		Qy	121 VILHDSRKRSSEAAKGPV-KPTYNSPFPYCKGPCHKVQGTCRQATLTLAQGP
PD 07-MAR-2001..		Db	121 VILHDSRKRSSEAAKGPV-KPTYNSPFPYCKGPCHKVQGTCRQATLTLAQGP
XX PR 30-AUG-1999; 99EP-00116766.		Qy	181 SCWDDVLIPNRMSCGECQSPICPGTSAEFFFKCGAHPTSDKETPVALKHTATSRNITCIT
PA (BIOF-) BIOFRONTERA PHARM GMBH.		Db	180 SCWDDVLIPNRMSCGECQSPICPGTSAEFFFKCGAHPTSDKETPVALKHTATSRNITCIT
P1 Luebbert H;		Qy	241 CTDVRSPVLFVQCNHRHVICLDFCHLYCVTRLNDROFVHDPOLGYSUPCVAQCPNSLIKE
XX DR WPI: 2001-212797/22.		Db	240 CTDVRSPVLFVQCNHRHVICLDFCHLYCVTRLNDROFVHDPOLGYSUPCVAQCPNSLIKE
XX DR N-PSDB; AAFF5258.		Qy	301 LHHRFLIGEQQYNYQYQGAEBCVLQMGGLCPRPGCGAGLIPEDQPKVTEBGGNGLGC
PT New polynucleotides encoding mouse parkin2 protein, useful for producing		Db	300 LHHRFLIGEQQYNYQYQGAEBCVLQMGGLCPRPGCGAGLIPEDQPKVTEBGGNGLGC
RESULT 9		SO	Sequence 464 AA;
AAB67532		Query Match	83.4%; Score 2165.5; DB 4; Length 464;
ID AAB67532	standard; protein; 464 AA.	Best Local Similarity	83.2%; Pred. No. 1-78-181;
AC AAB67532;		Matches	29; Mismatches 48; Indels 1; Gaps 1;
XX DT 29-MAY-2001 (first entry)		Qy	1 MIVFVRNSHGGPPVEVDTSIFOLKEVAKRQGPADQRVIFAGKEIRNDWTVQND
DB DE Amino acid sequence of a mutated murine parkin2 polypeptide.		Db	1 MIVFVRNSHGGPPVEVDTSIFOLKEVAKRQGPADQRVIFAGKEIRNDWTVQND
XX KW Parkinson2; Parkinson's disease; 6q25.2-27; neurodegenerative disease; Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis; Multi-system atrophy; Wilson's disease; Pick's disease; Prion disease; brain tumour; head trauma; stroke; vascular irregularity; metabolic irregularity.		Qy	61 LDQOSIVHIVPWRPKQGMNATGGDPRAAGGEREPOSLTRVDSLSSVLPDSVGLA
OS Mus sp.		Db	61 LDQOSIVHIVPWRPKQGMNATGGDPRAAGGEREPOSLTRVDSLSSVLPDSVGLA
XX PN EP1081225-A1.		Qy	121 VILHDSRKRSSEAAKGPV-KPTYNSPFPYCKGPCHKVQGTCRQATLTLAQGP
PD 07-MAR-2001..		Db	121 VILHDSRKRSSEAAKGPV-KPTYNSPFPYCKGPCHKVQGTCRQATLTLAQGP
XX PR 30-AUG-1999; 99EP-00116766.		Qy	181 SCWDDVLIPNRMSCGECQSPICPGTSAEFFFKCGAHPTSDKETPVALKHTATSRNITCIT
PA (BIOF-) BIOFRONTERA PHARM GMBH.		Db	180 SCWDDVLIPNRMSCGECQSPICPGTSAEFFFKCGAHPTSDKETPVALKHTATSRNITCIT
P1 Luebbert H;		Qy	241 CHVVEKGNGCMMHKCPQPQCKLEWCMNGCEWNRVCMGDHWFDV
XX DR WPI: 2001-212797/22.		Db	240 CHVVEKGNGCMMHKCPQPQCKLEWCMNGCEWNRVCMGDHWFDV
XX DR N-PSDB; AAFF5258.		Qy	301 LHHRFLIGEQQYNYQYQGAEBCVLQMGGLCPRPGCGAGLIPEDQPKVTEBGGNGLGC
PT New polynucleotides encoding mouse parkin2 protein, useful for producing		Db	300 LHHRFLIGEQQYNYQYQGAEBCVLQMGGLCPRPGCGAGLIPEDQPKVTEBGGNGLGC

XX OS Mus sp.
 XX PN EP1081225-A1.
 XX PD 07-MAR-2001..
 XX PP 30-AUG-1999; 99EP-00116766.
 XX PR 30-AUG-1999; 99EP-00116766.
 XX PA (BIOP-) BIOFRONTERA PHARM GMBH.
 XX PI Luebbert H;
 XX WPI: 2001-212797/22.
 DR N-PSDB; AAF55259.
 PT New polynucleotides encoding mouse parkin2 protein, useful for producing a transgenic non-human animal as an animal model for neurodegenerative diseases.
 XX PS Claim 7; Page 49-51; 62pp; English.
 CC The present sequence represents a murine parkin2 polypeptide. The sequence contains the mutation Thr415Asn. Mutations or deletions in the parkin2 gene cause Parkinson's disease in humans. The human parkin2 gene is located in gene region 6q25.2-27. Parkin2 polypeptides and polynucleotides are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, Multi-system atrophy, Wilson's disease, Pick's disease, Prion disease, and secondary causes inducing Parkinson's syndromes like toxins, drugs, brain tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated with a less active or non-active parkin protein.
 CC
 XX SQ Sequence 464 AA:
 Query Match 83.4%; Score 2165.5; DB 4; Length 464;
 Best Local Similarity 83.2%; Pred. No. 1.7e-181;
 Matches 387; Conservative 29; Mismatches 48; Indels 1; Gaps 1;
 CC
 Qy 1 MIVFVRPNSSGHPVPEVDSDTSIFOLKEVAKRQGVPADELRVIFAGKELRNDFWVQCD 60
 Db 1 MIVFVRPNSSGHPVPEVDSDTSIFOLKEVAKRQGVPADELRVIFAGKELRNHLTVQNC 60
 Qy 61 LDQOSTVHIVORPWRKGQEMATGGDPRAAGCEREPQLTRVDSLSSVLPGSVGLA 120
 Db 61 LEQOSTVHIVORPWRKGQEMATGGDPRAAGCEREPQLTRVDSLSSVLPGSVGLA 120
 Qy 121 VILHTDSRKUSPPAGSPAGSISYNSPYVYCKGPQCORVQPGKURVOCSTCROATLTQGP 180
 Db 121 VILHTDSRKUSPPAGSPAGSISYNSPYVYCKGPQCORVQPGKURVOCSTCROATLTQGP 180
 181 SCWDDVLIPNMRSGECOSPRCGTSAAFFKKGAHPTSDKETPVALHLMNRNCT 240
 Db 180 SCWDDVLIPNMRSGECOSPDGFGTRAFFKKGAHPTSDKOTSVVALNLTSNRRSPCIA 239
 Qy 241 CTDVRSPLVUQCNSHVICDCPHLYCVTRNDPFLQGSLIPCVAGCPNLSIKE 300
 Db 240 CTDVRSPVLVQCNHRHVICDCPHLYCVTRNDPFLQGSLIPCVAGCPNLSIKE 299
 Qy 301 LHHPRLIGEBOQWRYQOYGAEECVLQMGGVICPRPGGAGLILEPDPDKRVTCEGGNGLC 360
 Db 300 LHHPRLIGEBOQWRYQOYGAEECVLQMGGVICPRPGGAGLILEPDPDKRVTCEGGNGLC 359
 Qy 361 GFAFCBCKEAYHEGECSAVFEEASGTTQAYRDERAEQARWEAASKETTKTKPCPR 420
 Db 360 GFVFVCRDCKEAYHEGCDSDLLEPSGATSQAYRVFDKERAQEQRWEASKETTKTKPCPR 419
 Qy 421 CHVPVKEKNGGCHMKGCPQPCRLEWCWNCGCEWWNRVCMGDFHFDV 465

Db 420 CNVPIERGGCHMKGCPQPCRLEWCWNCGCEWWNRVCMGDFHFDV 464
 RESULT 10
 AAB67533 standard; protein; 451 AA.
 ID AAB67533
 XX
 AC AAB67533;
 XX DT 29-MAY-2001 (first entry)
 XX DE Amino acid sequence of a mutated murine parkin2 polypeptide.
 XX KW Parkinson; Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis; Multi-System atrophy; Wilson's disease; Pick's disease; Prion disease; brain tumour; head trauma; stroke; vascular irregularity; metabolic irregularity.
 XX OS Mus sp.
 XX PI Luebbert H;
 XX WPI: 2001-212797/22.
 DR N-PSDB; AAF55259.
 PT New polynucleotides encoding mouse parkin2 protein, useful for producing a transgenic non-human animal as an animal model for neurodegenerative diseases.
 XX PS Claim 7; Page 51-53; 62pp; English.
 CC The present sequence represents a murine parkin2 polypeptide. The sequence contains the mutation Trp453Stop. Mutations or deletions in the parkin2 gene cause Parkinson's disease in humans. The human parkin2 gene is located in gene region 6q25.2-27. Parkin2 polypeptides and polynucleotides are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, Multi-system atrophy, Wilson's disease, Pick's disease, Prion disease, and secondary causes inducing Parkinson's syndromes like toxins, drugs, brain tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated with a less active or non-active parkin protein.
 CC
 XX SQ Sequence 451 AA:
 Query Match 80.4%; Score 2087.5; DB 4; Length 451;
 Best Local Similarity 83.2%; Pred. No. 1.2e-174;
 Matches 376; Conservative 29; Mismatches 46; Indels 1; Gaps 1;
 CC
 Qy 1 MIVFVRPNSSGHPVPEVDSDTSIFOLKEVAKRQGVPADELRVIFAGKELRNDFWVQCD 60
 Db 1 MIVFVRPNSSGHPVPEVDSDTSIFOLKEVAKRQGVPADELRVIFAGKELRNHLTVQNC 60
 Qy 61 LDQOSTVHIVORPWRKGQEMATGGDPRAAGCEREPQLTRVDSLSSVLPGSVGLA 120
 Db 61 LEQOSTVHIVORPWRKGQEMATGGDPRAAGCEREPQLTRVDSLSSVLPGSVGLA 120
 Qy 121 VILHTDSRKUSPPAGSPAGSISYNSPYVYCKGPQCORVQPGKURVOCSTCROATLTQGP 180

Db 121 VILDTDSRKDRSEARGPV-KPTVNSFFIYCKCPCHKVQPGKLRVQCGTCKATLTLAQP 179
Qy 181 SCMDDVLLPNRMSGECOSPHCIGTSARFFPGKAHPDSKEPVHALIATNSRNITCT 240
Db 180 SCDDVLVLPNRMGECOSPCDPCPOTRAFFPGKAHPDSKOTSVANLNTSNSRPICTA 239
Qy 241 CTDVRSPLVFOCNRSRVICDCPHLYCVTRIANDROFVHDQLGSLIPCVAGCPNSLIKE 300
Db 240 CTDVRSPLVFOCNHRHVICDCPHLYCVTRIANDROFVHDQLGSLIPCVAGCPNSLIGE 299
Qy 301 LHFRILGEQMYRQYQGAECVLOMGGVLCPRPGGAGLIPERDORKVTCCEGNGLGC 360
Db 300 LHFRILGEQMYRQYQGAECVLOMGGVLCPRPGGAGLIPERDORKVTCCEGNGLGC 359
Qy 361 GFARCRECKEAYHEGECASAVTEASGTTQAVRUDERAEORWERASKETIKKTPKPCR 420
Db 360 GFVFCRDKCKEAYHEGCDLSLEPSGATSOVAVRUDERAEORWERASKETIKKTPKPCR 419
Qy 421 CHVPEVKNGGMHMCKCOPQRLEWCWNCC 452
Db 420 CNVP1BKNGGMMKCPQPKLEWCWNCGC 451

RESULT 11

ID ABO07158
XX ABO07158 standard; protein; 316 AA.

AC ABO07158;

XX

DT 13-AUG-2003 (first entry)

XX Human p53 modifying protein, SEQ ID 118.

DE Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic; antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer; lung cancer; ovarian cancer; angiogenesis; cell cycle; apoptotic disorder; cell proliferation disorder.

KW Homo sapiens.

OS Homo sapiens.

XX WO2002912-A1.

XX WO2002912-A1.

PD 12-DEC-2002.

PP 03-JUN-2002; 2002WO-US017382.

PR 05-JUN-2001; 2001US-0296076P.

PR 10-OCT-2001; 2001US-0228605P.

PR 11-FEB-2002; 2002US-0357233P.

XX (EXEL-) EXELIXIS INC.

PA

XX

PS Example 2; Page 402-403; 678pp; English.

CC The invention relates to identifying (M1) a candidate p53 pathway modulating agent, by contacting an assay system comprising a purified HM polypeptide (human orthologue of genes that modify the p53 pathway in Drosophila) or nucleic acid with a test agent under conditions, where but for the presence of the test agent, the system provides a reference activity, and detecting a test agent-biased activity of the assay system. Also included are modulating (M2) a p53 pathway of a cell (comprising contracting a cell defectorlike in p53 function with a candidate modulator that specifically binds to a HM polypeptide comprising an HM amino acid

RESULT 11

ID ABO07158
XX ABO07158 standard; protein; 316 AA.

AC ABO07158;

XX

DT 13-AUG-2003 (first entry)

XX Human p53 modifying protein, SEQ ID 118.

DE Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic; antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer; lung cancer; ovarian cancer; angiogenesis; cell cycle; apoptotic disorder; cell proliferation disorder.

KW Homo sapiens.

OS Homo sapiens.

XX WO2002912-A1.

XX WO2002912-A1.

PD 12-DEC-2002.

PP 03-JUN-2002; 2002WO-US017382.

PR 05-JUN-2001; 2001US-0296076P.

PR 10-OCT-2001; 2001US-0228605P.

PR 11-FEB-2002; 2002US-0357233P.

XX (EXEL-) EXELIXIS INC.

PA

XX

PS Example 2; Page 402-403; 678pp; English.

CC The invention relates to identifying (M1) a candidate p53 pathway modulating agent, by contacting an assay system comprising a purified HM polypeptide (human orthologue of genes that modify the p53 pathway in Drosophila) or nucleic acid with a test agent under conditions, where but for the presence of the test agent, the system provides a reference activity, and detecting a test agent-biased activity of the assay system. Also included are modulating (M2) a p53 pathway of a cell (comprising contracting a cell defectorlike in p53 function with a candidate modulator that specifically binds to a HM polypeptide comprising an HM amino acid

RESULT 12

ID AAB67521
XX AAB67521 standard; protein; 344 AA.

AC AAB67521;

XX

DT 29-MAY-2001 (first entry)

XX Amino acid sequence of a murine truncated parkin2 polypeptide.

CC Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease; Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis; Multi-system atrophy; Wilson's disease; Pick's disease; Prion disease;

CC

Sequence 316 AA:

Query	Match	Score	DB	Length	
Best Local Similarity	65.4%	1666.5	6	316	
Matches	316	Conservative	0	Mismatches	0
Indels	149	Gaps	1		

Qy 1 MIVFPRFNSSHGFPVEVDSDTSFLQKVEVAKRQGVPAQDOLRVIFASKELRNUWTQND 60
Db 61 LDQQSIVHIVQRPWRKGQMNATGGDPNRNAAGCEREPQSLTRVDISSLPGDSVGLA 120
Qy 58 -----
Db 58 -----
Qy 121 VILHFDTSRKDSPPRAGSPAGRSIYNSFVWCKGPQRYVQPKLRLVQGSTCROATLTQGP 180
Db 58 -----
Qy 181 SCDDVLINRMSGECQSPHCPCTSARFFPGKAHPDSKEPVHALIATNSRNITCT 240
Db 58 -----
Qy 241 CTDVRSPLVFOCNRSRVICDCPHLYCVTRIANDROFVHDQLGSLIPCVAGCPNSLIKE 300
Db 92 CTDVRSPLVFOCNRSRVICDCPHLYCVTRIANDROFVHDQLGSLIPCVAGCPNSLIKE 151
Qy 301 LHFRILGEQMYRQYQGAECVLOMGGVLCPRPGGAGLIPERDORKVTCCEGNGLGC 360
Db 152 LHFRILGEQMYRQYQGAECVLOMGGVLCPRPGGAGLIPERDORKVTCCEGNGLGC 211
Qy 361 GFARCRECKEAYHEGECASAVTEASGTTQAVRUDERAEORWERASKETIKKTPKPCR 420
Db 212 GFARCRECKEAYHEGECASAVTEASGTTQAVRUDERAEORWERASKETIKKTPKPCR 271
Qy 421 CHVPEVKNGGMHMCKCOPQRLEWCWNCC 465
Db 272 CHVPEVKNGGMHMCKCOPQRLEWCWNCC 316

KW brain tumour; head trauma; stroke; vascular irregularity;
KW metabolic irregularity.
OS Mus sp.
PN BP1081225-A1.

XX 07-MAR-2001.
PD XX
PP 30-AUG-1999; 99EP-00116766.
XX 30-AUG-1999; 99EP-00116766.
PR (BIOF-) BIOFRONTERA PHARM GMBH.
PA (BIOF-) BIOFRONTERA PHARM GMBH.
PX Luebbert H,
PT WPI; 2001-212797/22.
DR N-PSDB; ARF55249.

XX New polynucleotides encoding mouse parkin2 protein, useful for producing a transgenic non-human animal as an animal model for neurodegenerative diseases.

PT XX
PS Claim 7; Page 40-41; 62pp; English.
XX The present sequence represents a murine parkin2 polypeptide. The polynucleotide sequence contains a deletion, leading to a truncated protein. Mutations or deletions in the parkin2 gene cause Parkinson's disease in humans. The human parkin2 gene is located in gene region 6q25.2-27. Parkin2 polypeptides and polynucleotides are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, multi-system atrophy, Wilson's disease, Pick's disease, prion disease, and secondary causes inducing Parkinson's syndromes like toxins, drugs, brain tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated with a less active or non-active parkin protein

SQ Sequence 344 AA:

Query Match 64.7%; Score 1679.5; DB 4; Length 344;
Best Local Similarity 66.0%; Pred. No. 6.3e-139;
Matches 307; **Conservative** 14; **Mismatches** 23; **Indels** 121; **Gaps** 1;

QY 1 MIVFVRNNSHGPVPEVDSDTISIQLKEVAKRQGVPAQDOLRVIAGKELRNNDWTQNCD 60
Db 1 MIVFVRNNSHGPVPEVDSDTISIQLKEVAKRQGVPAQDOLRVIAGKELRNNDWTQNCD 60
QY 61 LDQQSIVHIVORPWRKGQEMNTGGDPPRNAAGGCEREPQSLTRVLDLSSVLPGSVGLA 120
Db 57 ----- 56
QY 121 VLIHTSRKSDSPPGSPAGRSYIYNFSVYVCKPCQVRQPGKURQVQESTCROPLTITQGP 180
Db 57 ----- 59
QY 181 SCWDDVLIPNRMSGECOSPHEPGTSAAFFKQGAHPTSDKETPVHLIATNSRNITCIT 240
Db 60 SCWDDVLIPNRMSGECOSPHEPGTSAAFFKQGAHPTSDKETPVHLIATNSRNITCIT 240
QY 241 CTDVRSPLVFOCNRSHVICLCPFLYCVTRNDRDFVHDPOGLYSIPCVAGCPNSLIKE 300
Db 120 CTDVRSPLVFOCNRSHVICLCPFLYCVTRNDRDFVHDPOGLYSIPCVAGCPNSLIKE 179
QY 301 LHFRFLIGEONRYQOGABECVQGVLCPFLYCVTRNDRDFVHDPOGLYSIPCVAGCPNSLIKE 360
Db 180 LHFRFLIGEONRYQOGABECVQGVLCPFLYCVTRNDRDFVHDPOGLYSIPCVAGCPNSLIKE 239
QY 361 GFAFCRCKEAYHEGECSAVFERSGTITQAVFUDERAQAEQARWEASKEITKTKTPCPR 420
Db 240 GFVFRCRCKEAYHEGDCDSLEPSGATSQAVFUDERAQAEQARWEASKEITKTKTPCPR 299

XX RESULT 13
XX AAB67526
ID AAB67526 standard; protein; 296 AA.
XX 29-MAY-2001 (first entry)
DE Amino acid sequence of a murine truncated parkin2 polypeptide.

XX Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease; Alzheimer's disease; Huntingdon's disease; Amyotrophic lateral sclerosis; Multi-system atrophy; Wilson's disease; Pick's disease; Prion disease; brain tumour; head trauma; stroke; vascular irregularity; metabolic irregularity.

XX MUS SP.

OS PN
PN BP1081225-A1.
XX 07-MAR-2001.
PD XX
PP 30-AUG-1999; 99EP-00116766.
XX PR
PR 30-AUG-1999; 99EP-00116766.
PA (BIOF-) BIOFRONTERA PHARM GMBH.
PX Luebbert H,
PT WPI; 2001-212797/22.
DR N-PSDB; ARF55253.

XX New polynucleotides encoding mouse parkin2 protein, useful for producing a transgenic non-human animal as an animal model for neurodegenerative diseases.

PT XX
PS Claim 7; Page 44-45; 62pp; English.
XX The present sequence represents a murine parkin2 polypeptide. The polynucleotide sequence contains a deletion, leading to a truncated protein. Mutations or deletions in the parkin2 gene cause Parkinson's disease in humans. The human parkin2 gene is located in gene region 6q25.2-27. Parkin2 polypeptides and polynucleotides are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, multi-system atrophy, Wilson's disease, Pick's disease, prion disease, and secondary causes inducing Parkinson's syndromes like toxins, drugs, brain tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated with a less active or non-active parkin protein

SQ Sequence 296 AA:

Query Match 47.6%; Score 1234.5; DB 4; Length 296;
Best Local Similarity 80.0%; Pred. No. 7.3e-100;
Matches 232; **Conservative** 20; **Mismatches** 37; **Indels** 1; **Gaps** 1;

QY 1 MIVFVRNNSHGPVPEVDSDTISIQLKEVAKRQGVPAQDOLRVIAGKELRNNDWTQNCD 60
Db 1 MIVFVRNNSHGPVPEVDSDTISIQLKEVAKRQGVPAQDOLRVIAGKELRNNDWTQNCD 60
QY 61 LDQQSIVHIVORPWRKGQEMNTGGDPPRNAAGGCEREPQSLTRVLDLSSVLPGSVGLA 120
Db 61 LDQQSIVHIVORPWRKGQEMNTGGDPPRNAAGGCEREPQSLTRVLDLSSVLPGSVGLA 120
QY 61 LEQQSIVHIVORPWRKGQEMNTGGDPPRNAAGGCEREPQSLTRVLDLSSVLPGSVGLA 120
Db 61 LEQQSIVHIVORPWRKGQEMNTGGDPPRNAAGGCEREPQSLTRVLDLSSVLPGSVGLA 120

OY 121 VILHTDSRKDSPAGSPAGRSIYNPSVYCKPCQVQGKLRVQGSTCQATLTQGP 180
Db 121 VILDTDSRKDSRARGPV-KPTNPFYVCKPCPQGKLRVQGTCQATLAQGP 179
OY 181 SCWDDVLPNRMGECOPSPH-CPGTSABFFKGGAHPTSDKETPVVALHTATNSRITCT 240
Db 180 SCWDDVLPNRMGECOPSPH-CPGTSABFFKGGAHPTSDKETPVVALHTATNSRITCT 239
OY 241 CTDVRSPLVQNCNSRHIVCICDFCHIYCUTLNDROFVDRPOLGSLPCV 290
Db 240 CTDVRSPLVQNCNSRHIVCICDFCHIYCUTLNDROFVDRPOLGSLPCV 289

RESULT 14

ABB65114
ID ABB65114 standard; protein; 468 AA.
AC ABB65114;
XX DT 26-MAR-2002 (first entry)
DE Drosophila melanogaster polypeptide SEQ ID NO 22134.
KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
KW Drosophila melanogaster.
XX OS WO20011042-A2.
XX PD 27-SEP-2001.
XX PP 23-MAR-2001; 2001WO-US009231.
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX PA (PEKE) PB CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX DR WPI; 2001-65-6860/75.
DR N-PSDB; ABU9217.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
XX PS Disclosure; SEQ ID NO 22134; 21pp + Sequence Listing; English.
CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABU16176-ABU16175) and the encoded proteins (AB85737-AB2027). The sequence data for this pattern did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 468 AA;

Query Match Best Local Similarity 42.6%; Pred. No. 4e-84; Length 468; Matches 201; Conservative 80; Mismatches 158; Indels 33; Gaps 9;

OY 3 VFVRENSHGFVFVEVDTSFVQLEVKVAKRQGVADQKRVFKKELANDWTVQNCOLD 62
Db 18 IVKVNIGKTIVTUVNLBQWQDVKVNLVAPOLQGDPDKITFAGKELSDATTIEQCDIG 77
OY 63 QSVIIVHQ-RPRWKQEMMAGGGDPDPRMAGGCEREPOLSTVRLSSVLPEDSVGLAV 121

RESULT 15

ARB67519
ID AAB67519 standard; protein; 250 AA.
AC AAB67519;
XX DT 29-MAY-2001 (first entry)
XX DB Amino acid sequence of a murine parkin2 polypeptide.
XX PA Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease; Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis; Multi-system atrophy; Wilson's disease; Pick's disease; Prion disease; brain tumour; head trauma; stroke; vascular irregularity; metabolic irregularity.
OS Mus sp.
XX PN EPI081225-A1.
XX PD 07-MAR-2001.
XX PP 30-AUG-1999; 99EP-00116766.
XX PR 30-AUG-1999; 99EP-00116766.
XX PA (BIOPT-) BIOPRONTERA PHARM GMBH.
XX PI Luebbert H;
XX DR WPI; 2001-212797/22.
DR N-PSDB; ABM55246.
XX PT New polynucleotides encoding mouse parkin2 protein, useful for producing a transgenic non-human animal as an animal model for neurodegenerative diseases.
XX PS Claim 7; Page 21-22; 62pp; English.
XX CC The present sequence represents a murine parkin2 polypeptide. Mutations or deletions in the parkin2 gene cause Parkinson's disease in humans. The human parkin2 gene is located in gene region 6q25.2-27. Parkin2 polypeptides and polynucleotides are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral

CC sclerosis, Multi-system atrophy, Wilson's disease, Pick's disease, Prion
 CC disease, and secondary causes inducing Parkinson's syndrome like toxins,
 CC drugs, brain tumours, head trauma, stroke, vascular irregularities or
 CC metabolic irregularities, associated with a less active or non-active
 CC parkin protein
 XX
 SQ sequence 250 AA;

Query Match 38 6%; Score 1002; DB 4; Length 250;
 Best Local Similarity 77.6%; Pred. No. 1.7e-79; Matches 190; Conservatiive 20; Mismatches 35; Indels 0; Gaps 0;
 Matches 190; Conservatiive 20; Mismatches 35; Indels 0; Gaps 0;

```

Qy 1 MIVFVRPNSSHGPFPYEVDSITSFOLKEVVAKROGVPAOLRVI FAGKQILRNDDWVQNC 60
Db 1 MIVFVRPNSSYGPFPYEVDSITSIOLKEVVAKROGVPAOLRVI FAGKQILPNHLTVQNC 60
Qy 61 LDQQSTVHTVQRPWRKGQEMMAITGGDPRMAGGEREPOPLTRVDSLSSVLPGDSVGLA 120
Db 61 LEQQSIVHIVQPRRSHETNAGGDEPQSTSEGSIWESRLTRDLSSTLPDSVGLA 120
Qy 121 VILHDPSRKOSPPAGSPAGRSIYNNSPVYVCKGKPCORVQPEKLRVOCSTRCATLTLTQGP 180
Db 121 VILDPSKRSEAAARGPAVKETTYNSPFYICKGKPCHKVQPGKLRVOCGTCKQATLTLAQGP 180
Qy 181 SCWDDVLIPRMMSGCOSPICPGTSAEFFKCGAMPTSDGETPVALHILNTSNRITCIR 240
Db 181 SCWDDVLIPRMMSGCOSPICPGTSAEFFKCGAMPTSDGETPVALHILNTSNRISPCIA 240
Qy 241 CTDVR 245
Db 241 CTDVR 245

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Om protein - protein search, using sw model

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(without alignment(s))
1341.256 Million cell updates/sec

Title: Perfect score: US-10-622-817-8

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs., 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /cgn2_6/pctdata/1/iaaa/6A_COMB.pep: *
- 3: /cgn2_6/pctdata/1/iaa/6B_COMB.pep: *
- 4: /cgn2_6/pctdata/1/iaaa/PCTUS_COMB.pep: *
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- 6: /cgn2_6/pctdata/1/iaaa/backFiles1.pep: *

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2596	100.0	465	US-09-601-844B-2
2	2596	100.0	465	US-09-601-844B-2
3	2405	92.6	437	US-09-601-844B-2
4	2405	92.6	437	US-09-601-844B-2
5	1966.5	65.4	316	US-09-949-016-6853
6	370.5	14.3	117	US-09-270-767-32183
7	240.5	9.3	503	US-09-91-259-13
8	222	5.6	474	US-09-354-221-2
9	222	8.6	487	US-09-949-016-1011
10	191	7.4	506	US-09-248-796A-15410
11	167	6.4	587	US-08-893-333-2
12	167	6.4	587	US-08-893-333-2
13	149	5.7	464	US-09-530-092-598
14	141	5.4	348	US-09-240-796A-16471
15	133	5.1	352	US-08-858-764-2
16	133	5.1	352	PCT-US95-09377-2
17	131.5	11.0	4	US-09-949-008A-2
18	130.5	5.0	1242	US-09-488-2708-2
19	128.5	4.9	229	US-08-726-3062-23
20	128.5	4.9	229	US-08-841-146-20
21	128.5	4.9	229	US-09-360-220-20
22	128	4.9	160	US-09-370-838-205
23	128	4.9	160	US-09-854-131-205
24	127	4.9	2321	US-09-230-652-2
25	126	4.9	237	US-09-248-796A-19062
26	126	4.9	846	US-08-149-103-3
27	126	4.9	846	US-08-451-883-3

ALIGNMENTS

RESULT 1
US-09-601-844B-2
Sequence 2, Application US/09601844B
; Pattern No. 6716621
; GENERAL INFORMATION:
; APPLICANT: Shimizu, No. 6716621uyoshi
; TITLE OF INVENTION: Isolated DNA or Gene Responsible for Parkinson's Disease
; FILE REFERENCE: 0652-211000
; CURRENT APPLICATION: US/09/601, 844B
; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: PCT/JFF99/00545
; PRIOR FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS.: 70
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 2
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-601-844B-2

Query Match 100.0%; Score 2596; DB 4; Length 465;
Best Local Similarity 100.0%; Pred. No. 8.4e-251; Indels 0; Gaps 0;
Matches 465; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIVFVRFNSHGFPEVSDSTSITOLKEVAKRKGQVPAQDQRVIAKGELENDWTYONCD 60
Db 1 MIVFVRFNSHGFPEVSDSTSITOLKEVAKRKGQVPAQDQRVIAKGELENDWTYONCD 60
QY 61 LDQOSIVHTVQRPWRKGQEMNATGGDPRNAGGEREPOSSLTRVLSSYLPGSVLA 120
Db 61 LDQOSIVHTVQRPWRKGQEMNATGGDPRNAGGEREPOSSLTRVLSSYLPGSVLA 120
QY 121 VILHTDSRKOSPPAGSPAGS 180
Db 121 VILHTDSRKOSPPAGSPAGS 180
QY 181 SCWDDVLIPRMSGCQSPCPGSAEFFKCGAHTPSDETPVHLIATNSRVCIT 240
Db 181 SCWDDVLIPRMSGCQSPCPGSAEFFKCGAHTPSDETPVHLIATNSRVCIT 240
QY 301 LHRHFRILGEEQNYQYGAECVLUQMGSYLCPRGCGAGLPLPERDORKYTCEGGLG 360
Db 301 LHRHFRILGEEQNYQYGAECVLUQMGSYLCPRGCGAGLPLPERDORKYTCEGGLG 360
QY 301 LHRHFRILGEEQNYQYGAECVLUQMGSYLCPRGCGAGLPLPERDORKYTCEGGLG 360

361 GFAFCRECKEAYHEGCSAVFBEASSTTQYRVDERAAQRWEASKETIKTTKPCP 420


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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6853
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6853

Query Match 92.6%; Score 2405; DB 4; Length 437;
Best Local Similarity 94.0%; Pred. No. 9.6e-232;
Matches 437; Conservative 0; Mismatches 0; Indels 28; Gaps 1;

Qy 1 MIVFVRPNSSHGPPEVSDTSIFOLKEVAKROGVPADOLRVAGKELRNDWTWONCD 60
Db 1 MIVFVRPNSSHGPPEVSDTSIFOLKEVAKROGVPADOLRVAGKELRNDWTWQ--- 57
Qy 61 LDQOSVHIVORPWRKGQEMNATGGDDPRMAGGCEREPOLTRVDLSSVLPGDSVGLA 120
Db 58 -----
Qy 181 SCWDVLLPNRMSGEQS PHRGTSAEFFPKGAIPTSDEKTPVALHLATNSRNITCIT 240
Db 58 -----
Qy 121 VILHTDSRKOSPPAGSPAGSISYNSPYVYCKGPQRCVQPGKLRVQCGSTCROATLTQGP 180
Db 121 VILHTDSRKOSPPAGSPAGSISYNSPYVYCKGPQRCVQPGKLRVQCGSTCROATLTQ-- 178
Qy 181 SCWDVLLPNRMSGEQS PHRGTSAEFFPKGAIPTSDEKTPVALHLATNSRNITCIT 240
Db 179 ----- EFFFKAHPDSKETPVALTHIATNSRNITCIT 212
Qy 241 CTDVRSPLVFOQNSRHVICDCPHIYCVTRLANDROPVHDQLGSLPCVAGCPNSLIKE 300
Db 213 CTDVSPVLPVFCNSRHVICDCPHIYCVTRLANDROPVHDQLGSLPCVAGCPNSLIKE 272
Qy 301 LHFRIGEEOYNRYQOYGAEECVLQMGVLCPRPGAGILPEPDQKVTCCEGNGLGC 360
Db 273 LHHFRIGEEOYNRYQOYGAEECVLQMGVLCPRPGAGILPEPDQKVTCCEGNGLGC 332
Qy 361 GFAFCRECKEAYHEGCSAVFEASGTTQAYRUDERAEQARWEASKETIKTTKPCPR 420
Db 333 GFAFCRECKEAYHEGCSAVFEASGTTQAYRUDERAEQARWEASKETIKTTKPCPR 392
Qy 421 CHVPUVKNGGCMHKMCPQPCRLEWCWNCGGEWNRVCMGDHWFDV 465
Db 393 CHVPUVKNGGCMHKMCPQPCRLEWCWNCGGEWNRVCMGDHWFDV 437

RESULT 5
US-09-949-016-6854
; Sequence 6854, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32183
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6854

Query Match 14.3%; Score 370.5; DB 4; Length 117;
Best Local Similarity 53.3%; Pred. No. 3.8e-29;
Matches 64; Conservative 11; Mismatches 40; Indels 5; Gaps 2;
Qy 345 PDORKVTCCEGNGLGGPFAFCRECKEAYHEGCS- SAVFEASGTTQAYRUDERAEQARW 403
Db 1 PDCRKTKCN---GGYVFERNLOGYHGICLPCPGTGISATNSEYTVPNRAEARW 56
Qy 404 ERASKETIKTTKPCPRCHVPUVKNGGCMHKMCPQPCRLEWCWNCGGEWNRVCMGDHWFDV 463
Db 57 DEASNVTIKVSTKPCPKRPTERDGGCMEMVCTRAGGF EWCVQTCETWTRDCMGIAHWF 116
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6854
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6854

Query Match 65.4%; Score 1696.5; DB 4; Length 316;
Best Local Similarity 68.0%; Pred. No. 4.2e-161;
Matches 316; Conservative 0; Mismatches 0; Indels 149; Gaps 1;

RESULT 6
US-09-270-767-32183
; Sequence 32183, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Hamburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32183
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-270-767-32183

Query Match 14.3%; Score 370.5; DB 4; Length 117;
Best Local Similarity 53.3%; Pred. No. 3.8e-29;
Matches 64; Conservative 11; Mismatches 40; Indels 5; Gaps 2;
Qy 345 PDORKVTCCEGNGLGGPFAFCRECKEAYHEGCS- SAVFEASGTTQAYRUDERAEQARW 403
Db 1 PDCRKTKCN---GGYVFERNLOGYHGICLPCPGTGISATNSEYTVPNRAEARW 56
Qy 404 ERASKETIKTTKPCPRCHVPUVKNGGCMHKMCPQPCRLEWCWNCGGEWNRVCMGDHWFDV 463
Db 57 DEASNVTIKVSTKPCPKRPTERDGGCMEMVCTRAGGF EWCVQTCETWTRDCMGIAHWF 116
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6854
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-914-259-13
; Sequence 13, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES

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; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-914-259-13

Query Match 9, 3%; Score 240, 5; DB 4; length 503;
Best Local Similarity 27.5%; Pred. No. 3e-15; DB 4; length 503;
Matches 72; Conservative 42; Mismatches 11; Indels 37; Gaps 13;

Qy 209 PFKCGAHPSPDKETPVALHILATNRSNITCITCDVSPVLFQOCNSRHSRHICLDCPHLYC 268
Db 105 FFKC-AHVNPNAEAKIKTISRQECBECIFSLQPDPSMAGLGCGHPRCPMCHEYL 163

Qy 269 VTRLNDROFVHDPOGLYSLPCVA-GCPNSLKEHLHRILGEBOYN-RYQYGAECVUQ 326
Db 164 STK-----IVAGELQQTISCAHGC-DILVDDVTANLVTDARPVKVQQLINSFV-E 215

Qy 327 MG3VLI-CPPRGCG-AGLIPEDPDKRTCEGGNGLGGFAFCRECKEAVIEHG-ECASYE 382
Db 216 CNGLRLRWCPSPVDTYAVKPVAPRRVHK-----CGHVFACAGENWHDPVKCRWL-- 267

Qy 383 ASGTTTQAYRVDRRAAQARWMAASKETIKKITKPCPRCHVPUVERGSGNMKCPQPCR 442
Db 268 -----KQWIKKCDDDSSETSNIAAN-----TKQPCRSVITKDGGENHNWCKNQCK 315

Qy 443 LWMCWNCGCEMNVRVCMGDHWFD 464
Db 316 NBFCWVCLGSWP-HGSSWN 335

RESULT 8
US-09-354-221-2

; Sequence 2, application US/09354221
; Patent No. 6699714

; GENERAL INFORMATION:
; APPLICANT: Chang, Chawshang
; TITLE OF INVENTION: Androgen Receptor Coactivators
; FILE REFERENCE: 920930.90011
; CURRENT APPLICATION NUMBER: US/09/354,221
; CURRENT FILING DATE: 1999-07-15
; EARLIER APPLICATION NUMBER: US 60/100,243
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-354-221-2

Query Match 8, 3%; Score 240, 5; DB 4; length 474;
Best Local Similarity 27.3%; Pred. No. 3e-15; DB 4; length 474;
Matches 72; Conservative 42; Mismatches 11; Indels 37; Gaps 13;

Qy 232 NSRNITC-ITCTDVRSPVLF-QCNSRHTCILDCPHLYCVTRNLDRFVHDPOGLYSLP 288
Db 227 NSKLFLGSCIFCBEKLGSSECMLFLEC--RHYVKAICLVDYFBIORDGQ-----VQ 274

Qy 289 CVAGCPN-----SLIKEHLHRILGEBOYN-RYQYGAECVUQ 338
Db 275 CL-NCPEPKCPSPVATPGQVKEL---VEAFLARYDRILLQSLDMLADWVVCPRPCQ 328

Qy 339 AGSLIPEDPDKRTCEGGNGLGGFAFCRECKEAVIEHG-ECASYE 382
Db 329 LEVMOERG-----CTMGCGCSCNFACTLGRILTHGVPCPKVTAKEKMDRNLYQDA 383

Qy 392 -----RVDRRAAQARWMAASKETIKKITKPCPRCHVPUVERGSGNMKCPQPCR 442
Db 384 NKRLLDORYGKRVIQKALEMSEKWELEGNSKSCPCGTPIEKLDGKNTC-TGCMQY 441

Qy 445 WCMWCGERWRCMG 459
Db 442 FCW-----ICMG 448

RESULT 9
US-09-949-016-1011
; Sequence 1011, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CI00107
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10111
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-1011

Query Match 8, 6%; Score 222; DB 4; length 487;
Best Local Similarity 27.8%; Pred. No. 2e-13; DB 4; length 487;
Matches 71; Conservative 27; Mismatches 97; Indels 60; Gaps 13;

Qy 232 NSRNITC-ITCTDVRSPVLF-QCNSRHTCILDCPHLYCVTRNLDRFVHDPOGLYSLP 288
Db 227 NSKLFLGSCIFCBEKLGSSECMLFLEC--RHYVKAICLVDYFBIORDGQ-----VQ 274

Qy 289 CVAGCPN-----SLIKEHLHRILGEBOYN-RYQYGAECVUQ 338
Db 275 CL-NCPEPKCPSPVATPGQVKEL---VEAFLARYDRILLQSLDMLADWVVCPRPCQ 328

Qy 339 AGSLIPEDPDKRTCEGGNGLGGFAFCRECKEAVIEHG-ECASYE 382
Db 329 LEVMOERG-----CTMGCGCSCNFACTLGRILTHGVPCPKVTAKEKMDRNLYQDA 383

Qy 392 -----RVDRRAAQARWMAASKETIKKITKPCPRCHVPUVERGSGNMKCPQPCR 442
Db 384 NKRLLDORYGKRVIQKALEMSEKWELEGNSKSCPCGTPIEKLDGKNTC-TGCMQY 441

Qy 445 WCMWCGERWRCMG 459
Db 442 FCW-----ICMG 448

RESULT 10
US-09-248-796A-15410
; Sequence 1510, Application US/09248796A
; Patent No. 674737

; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15410
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-15410

Query Match 7.4%; Score 191; DB 4; Length 506;
Best Local Similarity 23.6%; Pred. No. 2.7e-10;
Matches 79; Conservative 48; Mismatches 118; Indels 90; Gaps 17;

Qy 166 CSTCRGATLTTTGTGSPCWWDDVILIPNRMMSGECOPSPHRCRTSABER-FFKCGAHPTSDKETPVA 225
Db 207 CDIC-OXTL--KGHLG-----TKFDSCGHVFNCNLAYEFESC----- 241

Qy 226 LHLIATNSRNITCITCTDVRSPVLVQFQNSRHHVICDFCHYCVTRLNIRFOFHPHQLY 285
Db 242 ---TESGDIDKVKHEPD-----PECTKVYKVKKKF-MELLETWHRNDKVKOMLNQ 288

Qy 286 SLPVCVAGCPNSLKELHHFRIGEQQNYQ---OYGABECVUQMGGLCPRGGAGLLP 343
Db 289 LIPSI--PLAMTKLKPSLVDRYVNLFKKSQYEWIGNILPNRLJKCPRVGCBVIR 345

Qy 344 EP-DORKTCISGNGLGCFCARFCRECKEAVIE-----GRCSAVFEASSTTORY--- 391
Db 346 EDIDEKLUVCP----KCKYACNDCRSKSYHARFKLUCLKINBNDKYLGIPIEDLEAPLL 400

Qy 392 -----RVDERAAEQARWEAAASKETI--KXITKPCPRCHVPPVERKNGGM 432
Db 401 PPDPSYDKKMINAKYGRKRID-RAIEYQMDPQFQMRERKTVWQPGCSATENSGCN 459

Qy 433 HKMKCPOPOCRLEWCWNGCEMNRVCMG-----DEWFD 464
Db 460 KNKC--SLICKDPFCFNCGSK----IGNNHDFV 487

RESULT 11
US-00-398-008A-2
; Sequence 2, Application US/08398008A
; Patent No. 5465588
; GENERAL INFORMATION:
; APPLICANT: Kornbluth, Jacki
; TITLE OF INVENTION: DNA Encoding Natural Killer Lytic Associated
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gilbreth & Adler, P.C.
; STREET: 801 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: MACINTOSH Ici
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,008A
; FILING DATE: March 2, 1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/126,501
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Dr. Benjamin Aaron
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5705CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 777-3321
; TELEFAX: (713) 777-6908
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
; LENGTH: 587
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; HYPOTHETICAL: No
; ANTI-SENSE: No

Query Match 6.4%; Score 167; DB 1; Length 587;
Best Local Similarity 24.2%; Pred. No. 8.4e-08;
Matches 80; Conservative 24; Mismatches 114; Indels 112; Gaps 20;

Qy 178 OGPSCMDVILIPNRMMSGECOPSPHRCRTSABER-FFKCGAHPTSDKETPVA 236
Db 73 QGPP-----PEALPAE-----PAAEAAEAAAGAEGPFDDE-AAGGGPGGEV 117

Qy 237 TCITC---TIVRSPLVQFQNSRHHVICDFCHYCVTRLNIRFOFHPHQLY 274
Db 73 OGPP-----PEALPAE-----PAAEAAEAAAGAEGPFDDE-AAGGGPGGEV 117

Qy 275 -RQFVHDPLQGYSLPCVAGCPNSLKELHHFRIGEQQNYQYQQGAECVUQMGGLC 333
Db 175 IRILLADPPL-----MHKV-----DEPVVYLAQPDCL-----RWCP 207

Qy 334 RPPCGAGLIL-----PEPDORKTVCEGGNGLGCFCARFCRECKEAVIEHEGRCSAVFEASGT 386
Db 208 APDCGYAVIAVGASC-----KLTCTERE--GCOTEFCHICKQQTCDM--ARQQ 257

Qy 387 TTOQAVYDERRAAEQARWEAAASKETIKTTKPCPRCHVPPVERKNGGM--NGCMMHMKCPOQPCRLE 444
Db 258 RAOTLVRTRKHTSGLSY---GOESGPDDIKPCPRCSAYYIIKONDGSCHNMTC--AVCGCE 312

Qy 445 WCWNCC-----GC-----EWNR 455
Db 313 FOWLCMKIESDLHVLSPGCTFWGKKPWSR 342

RESULT 12
US-08-893-333-2
; Sequence 2, Application US/08893333A

; Patent No. 5581705

; GENERAL INFORMATION:

; APPLICANT: Kornbluth, Jacki

; TITLE OF INVENTION: DNA Encoding Natural Killer Lytic Associated Protein

; FILE REFERENCE: D5705CIP/D

; CURRENT APPLICATION NUMBER: US/08/893,333A

; CURRENT FILING DATE: 1997-07-16

; NUMBER OF SEQ ID NOS: 17

; SEQ ID NO 2

; LENGTH: 587

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Amino acid sequence of Natural Killer Lytic

; OTHER INFORMATION: Associated protein encoded by nucleotides

; OTHER INFORMATION: 190 to 1953 of Sequence ID. No. 5981705 1

; Patent No. 5981705

; US-08-893-333-2

Query Match 6.4%; Score 167; DB 2; Length 587;

Best Local Similarity 24.2%; Pred. No. 8.4e-08;

Matches 80; Conservative 24; Mismatches 114; Indels 112; Gaps 20;

Qy 178 OGPSCMDVILIPNRMMSGECOPSPHRCRTSABER-FFKCGAHPTSDKETPVA 236
Db 73 QGPP-----PEALPAE-----PAAEAAEAAAGAEGPFDDE-AAGGGPGGEV 117

Qy 237 TCITC---TIVRSPLVQFQNSRHHVICDFCHYCVTRLNIRFOFHPHQLY 274
Db 118 ECPLCIVRLPPEAPLL--SCPHRCRDLHTRLEIRESRVPISTCPCSERLNPHD 174

QY 275 -RQFVHDPQLYSLPCVAGCNSLKLHFRILGEQNYQQGABECCVLQMGVILCP 333 ; GENERAL INFORMATION:
Db 175 IRLIADPPL-----MHX---EEFTFVRLASDFDC----RWCP 207 ; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196-132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIORITY NUMBER: US 60/074,725
; PRIORITY FILING DATE: 1991-02-13
; PRIORITY APPLICATION NUMBER: US 60/096,409
; PRIORITY FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO: 16471
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-538-092-598
; Sequence 538, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIORITY NUMBER: 60/127,352
; PRIORITY FILING DATE: 1998-04-01
; PRIORITY APPLICATION NUMBER: 60/178,965
; PRIORITY FILING DATE: 2000-02-01
; SOFTWARE: CirapatSeqFormatter Version 0.9
; SEQ ID NO: 598
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number YML068W
; US-09-538-092-598
Query Match Best Local Similarity 5.7%; Score 149; DB 4; Length 464;
Matches 59; Conservative 33; Mismatches 105; Indels 78; Gaps 13;
QY 235 NITCITCTVRSPVLFQ-----CNSRHVICDCHIYCVRFLNDRQF--VHDPLGYS- 286 ; Query Match
Db 177 NYHCICMEMKGVRMILKPCHEANVHRYLCHGCAKSYFTAMIQENRISSVRCPOCYKE 236 ; Best Locl. Similarity 5.4%; Score 141; DB 4; Length 328;
; Sequence 2, Application US/08854764
; Parent No. 610300
; GENERAL INFORMATION:
; APPLICANT: Innes, Michael
; APPLICANT: Craey, Abla
; TITLE OF INVENTION: Production of Tissue Factor Pathway
; TITLE OF INVENTION: Inhibitor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton St.
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94508
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,764
; FILING DATE: 12-MAY-1997
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/286,530
; FILING DATE: 05-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Saveride, Paul B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0991.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2585
; TELEFAX: 510-655-3342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
RESULT 14
US-09-248-796A-16471
; Sequence 16471, Application US/09248796A
; Patent No. 6747137

US-08-854-764-2

Query Match 5.1%; Score 133; DB 3; Length 352;
 Best Local Similarity 18.3%; Pred. No. 0.0001; Mismatches 70; Conservative 56; MisMatches 116; Indels 140; Gaps 16;

Matches 70; Conservattive 56; Mismatches 116; Indels 140; Gaps 16;

Qy 1 MIVFRENSSGGFPVVEDSPSIFQKEVVAKRCYPAQDPRVIFAGKELRNWDWVNQCD 60
 Db 1 MQIFVKMLTGKTTLVESSTIDNVTSKIQDKEGIPPDQORLIFAGKCLRDGRTLSYN 60

Qy 61 LDQQSIVHIVRPWKQEMMTGGDPDRNAGGCEREPoSITRVLSSVLPGSVGLA 120
 Db 61 IQKBSTLHLVLR-----LRGGSEE-----DEEHTITDTDFLPFLK----- 97

Qy 121 VILHT--DSRKDPSPPAGSPACRSIYNSP-----VYV-----CKGPQRV 157
 Db 98 --MHSFCAFKADGPKAKMRFFENIFTROCEEFYGGCBGNQRPESELECKKWCTRD 155

Qy 158 QFGKLRVQCSCTCQATLTGQPSMDVLFNRMGSQCBH-CPGTSABFFK----- 211
 Db 156 NANRI-----IKTTLQBKEDFCFILE-----EDFGICRGYTRYFYNNOTKO 197

Qy 212 -----CGAHPTSKETPVVALIATNSRNITCITCDVRS 246

Db 198 CERPKYGGCLGMNNTFTELCKNICEDGPNQFQDVNYGQQLAVNN---SLTQSTKV 253

Qy 247 PVLVFOCNSRHVICLDCPH--LYCVT-----RLNDQFVHDOLGYSLP----- 288
 Db 254 PSL-FE-----FHGBSWCLTPADRGICRANENRFYNSVIGKCRPFKYSGCGGN 301

Qy 289 -----CVAGCPNSLIKEL 301
 Db 302 ENFTSKOECIACKKQFIORI 323

Search completed: February 23, 2005 14:01:03
 Job time : 27.8801 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 23, 2005, 13:57:26 ; Search time 73.0:13 Seconds
(without alignments)
2084.159 Million cell updates/sec

Title: US-10-622-817-8

Perfect score: 2595

Sequence: 1 MIVFVRFNSHGPVEVDS... CWNCCCBWRVCMDHWFDV 465

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

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3: /cgn2_6/prodata/1/pubpa/us06_new_pub.pep:*

4: /cgn2_6/prodata/1/pubpa/us05_pubcomb.pep:*

5: /cgn2_6/prodata/1/pubpa/us07_pubcomb.pep:*

6: /cgn2_6/prodata/1/pubpa/us08_pubcomb.pep:*

7: /cgn2_6/prodata/1/pubpa/us09_pubcomb.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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Result No.	Score	Query Match Length	DB ID	Description
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15 233.5 9.0 585 15 US-10-424-599-147673 Sequence 147673,
16 224.5 8.6 648 15 US-10-425-114-63379 Sequence 63379, A
17 222 8.6 474 9 US-09-808-387-42 Sequence 42, Appl
18 222 8.6 474 14 US-10-442-754-2 Sequence 2, Appl
19 222 8.6 474 16 US-10-408-765A-572 Sequence 572, Appl
20 222 8.6 477 15 US-10-264-049-3019 Sequence 3019, Ap
21 219.5 8.5 1753 14 US-10-146-473-4 Sequence 44, Appl
22 219.5 8.5 1753 15 US-10-276-774-1824 Sequence 1824, Ap
23 219.5 8.5 2517 15 US-10-313-203-2 Sequence 2, Appl
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25 207.5 8.0 623 16 US-10-437-963-148905 Sequence 148905,
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ALIGNMENTS

RESULT 1

US-10-473-226-2

; Sequence 2, Application US/10473226
; Publication No. US20040198650A1

GENERAL INFORMATION:

APPLICANT: NeGene A/S

TITLE OF INVENTION: Means for inhibiting proteolytical processing of Parkin

FILE REFERENCE: 506-24-WO

CURRENT APPLICATION NUMBER: US/10-473,226

CURRENT FILING DATE: 2003-09-29

PRIOR APPLICATION NUMBER: DK PA 2001 00525

PRIOR FILING DATE: 2001-03-29

PRIOR APPLICATION NUMBER: US 60/281,286

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 2

LENGTH: 465

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: mat_peptide

NAME/KEY: mat_peptide

LOCATION: (1)..()

OTHER INFORMATION: Native Parkin

US-10-473-226-2

Query Match 100.0%; Score 2596; DB 16; Length 465;
Best Local Similarity 100.0%; Pred. No. 2.2e-220; Mismatches 0; Indels 0; Gaps 0;
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 RESULT 2
 US-10-776-604-2
 ; Sequence 2, Application US/10776604
 ; GENERAL INFORMATION:
 ; APPLICANT: Mizuno, Nobuyoshi
 ; TITLE OF INVENTION: DNAs or Genes Participating in Parkinson's Disease
 ; FILE REFERENCE: 0652.21/0001
 ; CURRENT APPLICATION NUMBER: US/10/776,604
 ; CURRENT FILING DATE: 2004-02-12
 ; PRIOR APPLICATION NUMBER: 09/601,844
 ; PRIOR FILING DATE: 2000-08-09
 ; PRIOR APPLICATION NUMBER: PCT/JP99/00545
 ; PRIOR FILING DATE: 1999-02-09
 ; PRIOR APPLICATION NUMBER: JP 10/17531
 ; NUMBER OF SEQ ID NOS: 81
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RESULT 4
US-10-473-226-4
; Sequence 4, Application US/10473226
; Publication No. US2004019850A1
; GENERAL INFORMATION:
; APPLICANT: NSGene A/S
; TITLE OF INVENTION: Means for inhibiting proteolytical processing of Parkin
; FILE REFERENCE: 506-204-WO
; CURRENT APPLICATION NUMBER: US/10/473, 226
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: DK PA 2001 00525
; PRIOR FILING DATE: 2001-03-29
; PRIORITY APPLICATION NUMBER: US 6/0/281, 286
; PRIOR FILING DATE: 2001-04-03
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1).()
; OTHER INFORMATION: Parkin with a D126E mutation
US-10-473-226-4

Query Match 99.5%; Score 2584; DB 16; Length 465;
Best Local Similarity 99.6%; Pred. No. 2.5e-219; Matches 463; Conservative 1; Mismatched 1; Indels 0; Gaps 0;
Matches 463; Conservative 1; Mismatched 1; Indels 0; Gaps 0;

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US-10-776-604-4
; Sequence 4, Application US/10776604
; Publication No. US200500335A1
; GENERAL INFORMATION:
; APPLICANT: Shimizu, Nobuyoshi
; APPLICANT: Mizuno, Yoshikuni
; TITLE OF INVENTION: DRGs or Genes Participating in Parkinson's Disease
; FILE REFERENCE: 0652_211001
; CURRENT APPLICATION NUMBER: US/10/776, 604
; CURRENT FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-785-548-4

Query Match 99.5%; Score 870; DB 9; Length 156;
Best Local Similarity 99.4%; Pred. No. 1.3e-68; Matches 155; Conservative 0; Mismatched 1; Indels 0; Gaps 0;

```

RESULT 7
US-10-239-249-2
; Sequence 2, Application US/10239249.
; Publication No. US20030177507A1
; GENERAL INFORMATION:
; APPLICANT: HONER, MARIUS
; APPLICANT: LINK, WOLFGANG
; APPLICANT: BAUMEISTER, RALF
; TITLE OF INVENTION: NEEMATOSES AS MODEL ORGANISMS FOR INVESTIGATING
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES AND, IN PARTICULAR, PARKINSON'S
; TITLE OF INVENTION: DISEASE, USES AND METHODS FOR FINDING SUBSTANCES AND
; TITLE OF INVENTION: GENES WHICH CAN BE USED IN TREATING SUCH DISEASES, AND
; TITLE OF INVENTION: IDENTIFICATION OF A NEEMATODE GENE
; FILE REFERENCE: 02481.1504-00000
; CURRENT APPLICATION NUMBER: US/10/239,249
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: PCT/EP01/03214
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 100 14 109.9
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-10-239-249-2

Query Match
Best Local Similarity 21.0%; Score 544.5; DB 14; Length 386;
Matches 129; Conservative 59; Mismatches 166; Indels 93; Gaps 13;
Qy 22 SIFOLKENVAKQHGGVADPQLRQYVAGGERPLRNWDTWQNCQDQSIHIVQRPWKRQEMN 81
Db 29 NIEDLTQDVKEKTEIPEDSELEVVFCGKLKSKSTIMRDLSLTATQMLRKFNSHNENG 88
Qy 82 ATGGDDPRNAAGGCERERPQLSLTRDLSVLPGDSVGLAVIHTDSRKDSPAGSPGRS 141
Db 89 AT-----TAKITTD-----S 99
Qy 142 IYNSSFYVCKGPQRVQPGKLRVQCSTCQATLTLTGQSPCMDWDVILPNRMGECOPSPHC 201
Db 100 ILGSFVWCKN-CDDYVRKGKURVYQKCSSTSIVLVSPEQWNSDVJKSKRIPAVCEBCT 158
Qy 202 PGTSAEFPFKCGAHPTSDKETVALVHILATNSRNTCTCTCDVDRSPVLUFOQNSRHVICL 261
Db 159 POLFASRKFKG---LACNDPAALHFLHRVGMWQMTICCCVCGKERYTIFDLCQ-HITCQ 212
Qy 262 DCFPHLYCVTRILNDRQTVHDOLGYSLPC-VAGCPNLSLIKELHHFRILGEBOYNRYQYGA 320
Db 213 FCFRDYLISOLERFGFVNQPHGFTFCPYGC-NRWVQDVFHFMQPSYEFORKAT 271
Qy 321 EECV.LQMGGLCIPRCGCCAGGLPER--DQKVTEEGNGLJCGFAFCRECKEAYHEGEC 377
Db 272 ERLIAVDDKGTCPCNNCGQSFWEYDDGCRSQCP----DCFFSFCRKC---FERNC 322
Qy 378 SAVFEASGTTQAVRVDERAEOARWEASKETTKTPCPRCVPUVEKNGGCMEMKCP 437
Db 323 VQCSEDLRTI-----TIDATRCPKCVATERINGGCAHHC- 360

RESULT 8
US-10-313-203-10
; Sequence 10, Application US/10313203
; Publication No. US20040029134A1
; GENERAL INFORMATION:
; APPLICANT: Gui, Wei
; APPLICANT: Nikolaev, Anatoly
; TITLE OF INVENTION: P53-ASSOCIATED PARKIN-LIKE CYTOPLASMIC PROTEIN, AND RELATED COMPOUNDS
; FILE REFERENCE: 68106
; CURRENT APPLICATION NUMBER: US/10/313, 203
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-313-203-10

Query Match
Best Local Similarity 14.4%; Score 373; DB 15; Length 64;
Matches 64; Conservative 100.0%; Bred. No. 3e-25; Mismatches 0; Indels 0; Gaps 0;
Qy 314 RQOQYGBECVQOMGGULCPREGCAGLLPPFDQKRVTCAGNGLGGFATCRECKEAYH 373
Db 1 RYQQYGBECVQOMGGVLCPREGCAGLLEPPFDQKRVTCAGNGLGGFAPCRECKEAYH 60
Qy 374 EGBC 377
Db 61 EGBC 64

Db

RESULT 9
US-10-313-203-17
; Sequence 17, Application US/10313203
; Publication No. US20040029134A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Wei
; APPLICANT: Nikolaev, Anatoly
; TITLE OF INVENTION: P53-ASSOCIATED PARKIN-LIKE CYTOPLASMIC PROTEIN, AND RELATED COMPOUNDS
; FILE REFERENCE: 68106
; CURRENT APPLICATION NUMBER: US/10/313, 203
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-313-203-17

Query Match
Best Local Similarity 12.4%; Score 323; DB 15; Length 56;
Matches 56; Conservative 100.0%; Bred. No. 6.7e-21; Mismatches 0; Indels 0; Gaps 0;
Qy 238 CTCCTDVRSPVLUFOQNSRHVICLCPFCFHLYCVTRILNDRQTVHDOLGYSLPCVAGC 293
Db 1 CITCTDVRSPVLUFOQNSRHVICLCPFCFHLYCVTRILNDRQTVHDOLGYSLPCVAGC 56

Db

RESULT 10
US-09-864-761-36750
; Sequence 36750, Application US/09864761
; Patent No. US20020049763A1
; GENERAL INFORMATION:

```

APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 FILE REFERENCE: Aeomica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 242633,6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Amnonax Sequence Listing Engine vers. 1.1
 SEQ ID NO: 36750
 LENGTH: 46
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AL035697.18
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.68
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.75
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.94
 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.63
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.68
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.91
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.77
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.73
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.96
 OTHER INFORMATION: EXPRESSED IN EST HUMAN HIT, EVALUATE 2.00E+00
 OTHER INFORMATION: SWISSPROT HIT: Q04833, EVALUE 9.10E-01
 US-09-864 - 761-36750
 Query Match 10.1%; Score 263; DB 9; Length 46;
 Best Local Similarity 100.0%; Fred. No. 1e-15; Mismatches 0; Indels 0; Gaps 0;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 312 YNRYQQYGAEBQVLOMQGVLCPRGCCAGLIEPDPDKVTCGGNG 357
 Db 1 VNRVQQYGAEECVLQmgGvICPRPGCCAGLIEPDPDKVTCGGNG 46
 RESULT 11
 US-10-437-963-199787
 Sequence 199787, Application US/10437963
 Publication No. US20040123333A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovacic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 APPLICANT: Wu, Wei
 APPLICANT: Boukharov, Andrey A.
 APPLICANT: Barbzuk, Brad
 APPLICANT: Li, Ping
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53221)B
 CURRENT APPLICATION NUMBER: US 10/437,963
 CURRENT FILING DATE: 2003-05-14
 NUMBER OF SEQ ID NOS: 204966
 SEQ ID NO: 199787
 LENGTH: 525
 TYPE: PRT
 ORGANISM: Oryza sativa
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT4530_95320C.1.pep
 US-10-437-963-199787
 Query Match 9.5%; Score 246; DB 16; Length 525;
 Best Local Similarity 30.1%; Pred. No. 7.1e-13; Mismatches 93; Indels 46; Gaps 11;
 Matches 71; Conservative 26; Mismatches 93; Indels 46; Gaps 11;
 Qy 232 NSRNNTCTCCTDVSPLVQFCNSRIVVICLQCFHLYCVTRNLNDROPVHDROGLYSFLPCV- 290
 Db 127 NRRRLCACTCVDFTGGMRSAGCSIFYCVSCWWRGV-----RAAVGDGARCLSRCPD 180
 Qy 291 ACCPNLSIKEJHFRILGEQYNRQOYGAEECVLQmgGV-LCPRGCCAGLIEPDPDKVTCGGNG 349
 Db 181 PSCPAAVVRREVLDVADGDR-ERIGFWFALSRSVVEBAGMRWCPSPGC-----SRA 230
 Qy 350 VTCEGGNG-----LGCGFAFCRC-KEAYHEGCSAVAEASGTTQAVRVDERAAEQ 400
 Db 231 VEFVGGDGESESSEVFCSCGHGLCWRCGEAHRPVSKTV-----AKWNEKSES 281
 Qy 401 --ARWAAASKTIKKTPKPCRHCVVVEKQGCMHMKCPOPOCRLEWCWNGCBBN 454
 Db 282 ETATWILAH-----TKRCKRKDRUDIEKQNGCMHMT-RPCLHBFCCWICLKPKW 329
 RESULT 12
 US-10-425-114-55407
 Sequence 55407, Application US/10425114
 Publication No. US2004034818A1
 GENERAL INFORMATION:
 APPLICANT: Liu, Jingdong
 APPLICANT: Zhou, Yihua
 APPLICANT: Kovacic, David K.
 APPLICANT: Screeen, Steven E
 APPLICANT: Tabaka, Jack E
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53313)B
 CURRENT APPLICATION NUMBER: US/10/425,114
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 73128
 SEQ ID NO: 55407
 LENGTH: 604
 TYPE: PRT
 ORGANISM: Glycine max
 FEATURE:
 OTHER INFORMATION: Clone ID: LIB3051-106-A7_FLI.pep

US-10-425-114-55407

Query Match 9.3%; Score 242.5; DB 15; Length 604;

Best Local Similarity 27.7%; Pred. No. 1.7e-12; Matches 70; Conservative 31; Mismatches 97; Indels 55; Gaps 12;

Qy 221 ETPVALHLATNSRNITCCTCDVRSPLVLFQCNRSRHVICLDPHLYCVTRNDQ--- 276
Db 140 EKPVFQN--SNTRBLTCGICGICPVEARVESTAGHPCYCWSWAGYFSTSINGPGCLV 196Qy 277 -FVFDPQLGYSPLCPVAGCNLSLKEHLHFRILGEQYQYQAEBCVLQMGV-LCPR 334
Db 197 LRCPDPS----CGAAVGQDMNLL----ASBDEKDQYDYLRSYEDNKKTKWCPA 245Qy 335 PGCGAGLIPERPDQKVTCGGNG----LGCGAFCREC-KEAYHEGCSAVFEASGT 388
Db 246 PGC-----EVAVTDAGSVDYDVSCLCCSYFCMCTEARHPVDC----GTIVS 289Qy 389 QAYRUDERAAEQRWEASKETIKTTKPCPCHVPEKNG3CMHMCKPQRQCRLWOWN 448
Db 290 KWIKLNKASESENMMW----ILANSKCPCKRPIEKNGCMHMTC-TPPCKFERCWL 341Qy 449 CGCEBNRVCMDH 461
Db 342 CLGAWS----DH 349RESULT 13
US-10-080-608A-13
; Sequence 13, Application US/10080608A
; Publication No. US20030198956A1
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/10/080_608A
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-10-080-608A-13US-10-370-685-102
Query Match 9.3%; Score 240.5; DB 15; Length 503;

Best Local Similarity 27.5%; Pred. No. 2.1e-12; Matches 72; Conservative 42; Mismatches 111; Indels 37; Gaps 13;

Qy 209 FFKCGAHPSDKETPVALLATNSRNITCCTCDVRSPLVLFQCNRSRHVICLDFHIC 268
Db 105 FFKA-AHVNPENATEAKQTSRSOCEBECIFQSOLPPDSMAGLECGHRFCMPCWHEYL 163Qy 269 VTRLADRQFFHDPLGYSPLCPVA-GCPNLSLIKELHFRILGEBOYN-RYQQYABECVLQ 326
Db 164 STK-----IVAGLIGOTISCAAHGC-DIIVDVTWANLTDAVRVYHQQLTNSFV-E 215Qy 327 MGGVIL-CIRPGCG-AGLILPEPDQKVTCGGNGLGCGFAFCBCKEAYHEG-ECSAVFE 382
Db 216 CNQLRWCVSVDCTYAVKPYAERRVICK----CGHVFCAFACGENWHDPVKCRM-L 267Qy 383 ASGTTQAYRUDERAAEQRWEASKETIKTTKPCPCHVPEKNG3CMHMCKPQRQCR 442
Db 268 -----KKWKKCDDSETSNWIAAN-----TKECPRSSVIEKGDGCHNMVKNONCK 315Qy 443 LEWCWNCGEGEWNRVCMDHFWD 464
Db 316 NEFCWVCLGGSWEP--HGSSWYN 335RESULT 15
US-10-424-592-147673
; Sequence 147673, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21 (53223B)
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 147673
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1..(585))
; OTHER INFORMATION: unsure at all xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_10436C.1.pep
; US-10-424-592-147673

RESULT 14

Query Match 9.0%; Score 233.5; DB 15; Length 585;

Best Local Similarity 26.5%; Pred. No. 1e-11; Matches 67; Conservative 29; Mismatches 102; Indels 55; Gaps 12;

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Qy  221 ETPVALHLATNSRNITCITCDVSPVLFQCNRSRHVICLDCFLYCVTRND---RQ 276
Db  120 EKPTVQH--PNAEITCGICFENYPRARLEMASCCHPYRISCTWEGCVISTSINDPGCLM 176
Qy  277 FVHDPOGLYSLPCVAGCPNSLIKELHHFRIGEEQNYQQYGAECVL-QMGGYLCPRP 335
Db  177 LSPPDKX-----CGAATGRS----SRFGSSSDEDIQKARYLNSYIENKKSTWCAP 225
Qy  336 GCGAGHLPEPDKVTCCEGN-----GLGCGFAFCREC-KEAVHGECSAWFEASGTT 388
Db  226 GC-----EYAVTFDAGSTIGNYDVSCLCSSYGFNCTEAHRPVDC-----GTVA 269
Qy  389 QAYRVDERAEQARMEASKEETIKITPKPCRCHVVEKONGCMIMMKCPQPQCLEWMWN 448
Db  270 KWILKNSAESAISNNW-----ILANSKPCERCKRTERKHGMIMTC-TPPCKKEFCWL 321
Qy  449 CGCEMWNRVCMDH 461
Db  322 CVGAMS-----DH 329

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Search completed: February 23, 2005, 14:33:24
 Job time : 75.0113 secs

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Om protein - protein search, using sw model

Run on: February 23, 2005, 13:34:50 ; Search time 19.3575 Seconds
 (without alignments)
 2311.294 Million cell updates/sec

Title: US-10-622-817-8

Perfect score: 2596

Sequence: 1 MIVFVRFINSSHGFPVEVDSD.....CWNCGCEWWNRVCMDHFWPDV 465

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqB, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR 79;*

- 1: pir1;*
- 2: pir2;*
- 3: pir3;*
- 4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description
1	490	18.9	T23460	hypothetical protein K08E3.7 - Caenorhabditis elegans
2	220	8.5	H84724	probable ARI-like
3	219.5	8.5	T00350	hypothetical prote
4	219.5	7.9	T16477	hypothetical prote
5	205	7.9	F07793	protein C27A12.6 [
6	198.5	7.6	T03366	hypothetical prote
7	196.5	7.6	GB4724	probable ARI-like
8	195	7.5	T5909	hypothetical prote
9	193	7.4	A8725	similar to Ariadne
10	190.5	7.3	A3626	protein C27A12.8 [
11	189	7.2	T31653	hypothetical prote
12	186.5	7.2	T6983	hypothetical prote
13	182.5	7.0	S28086	hypothetical prote
14	180.5	7.0	T04783	hypothetical prote
15	178.5	6.9	G87793	protein C27A12.7 [
16	178.5	6.9	B86448	hypothetical prote
17	174.5	6.7	T7498	hypothetical prote
18	174	6.7	T47498	hypothetical prote
19	173	6.7	F84721	probable RING zinc
20	162.5	6.3	J05983	protein kinase C-1
21	159	6.1	E84536	hypothetical prote
22	158.5	6.1	T16481	hypothetical prote
23	157	6.0	T9562	hypothetical prote
24	155	6.0	T07748	hypothetical prote
25	152.5	5.9	T55555	hypothetical prote
26	149	5.7	S48329	probable membrane
27	147	5.7	T52523	hypothetical prote
28	143.5	5.5	JH0226	ubiquitin / riboso
29	142.5	5.5	JH0226	ubiquitin / riboso

RESULT 1

T23460
 hypothetical protein K08E3.7 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #Sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T23460
 R;McMurray, A.
 Submitted to the EMBL Data Library, November 1996
 A;Reference number: 219743
 A;Accession: T23460
 A;Status: Preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-357 <WIL>
 A;Cross-references: UNIPROT:Q9XUS3; EMBL:281568; PIDN:CA04599.1; GSPDB:GN00021; CBSP:K08E3.7
 A;Experimental source: clone K08E3
 C;Genetics:
 A;Gene: CEPB;KO8B3.7
 A;Map position: 3
 A;Introns: 23/3; 72/2; 218/1; 286/2; 311/2

Query Match Best Local Similarity 18.9%; Score 490; DB 2; Length 357; Matches 119; Conservative 53; Mismatches 154; Indels 120; Gaps 12;

Qy 22 SFLQLKENVAKRQGVPAQDQLRIVFAGKELRNDWTVQNDLPOQSVIWHVQRPRWKQSGEMN 81
 Db 29 NIEDLTQKVEKULTEISDELETVFGKGLSKSTIMRLPDKNTATQIMLRLPKENSHNG 88

Qy 82 ATGGDDPPRNAAAGCEREPQLSLTRVLSSVLPGDSVGLAVIHTDSRKDSPPAGSPARS 141
 Db 89 AT-----TAKITDS-----S 99

Qy 142 IYNFSYYCKGPQCRQYQGPKLKVQFCQSTCRQATLTLTQGPSCWDDVLLPNRNSGECCSPHC 201
 Db 101 IIGSFYWMCKO-CDDYERKGKURVYQOKCSSTSLSVLVKSBNQWSDVLSKSR1PAVCBECT 158

Qy 202 POTSAAFFKQGAHPRTSDKEPVALPHLATNSRNITCTCDVRSPLVIFQNCNSRIVICL 261
 Db 159 PQLFAEKKPKC---LACNDPRAALTVRGHQMTQRCVQDCQKERYKTFIDGCN---HITCQ 212

Qy 262 DCFHLVYVTRLNDQFVHDPLQLGYSLPCVAGCPNSLKLHMPRLQEQNYQQGAE 321
 Db 213 FCFRV-----RIVQDVHIFHMGQTSEYORKATE 243

Qy 322 ECV-LQMGVQICPRPGGGAGLPEP--DQRKVTCEGGNGLGGCFAFCRECKEYAHGECS 378
 Db 244 RLIAVDDKGVTCPNVSCQSFWEPIDDGRSQCP---DCFFSFCKRC---FERNV 294

Qy 379 AVFEASCTTQAYVRDERRASQARWASKEETIKKTPKPCPRCHVAYVEKONGSCMMHCPQ 438
 Db 295 COSEDDLRT-----TIDATRRCRKHVATERNGCAHHHC-- 331

QY 439 PQCRLEWCWNCNGCENNRVNGDHWFD 464
Db 332 TSCGMWDWFCKTKEKECQWDHWFN 357

RESULT 2

H84724 probable ARI-like RING zinc finger protein [imported] - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Accession: H84724 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

R-Jin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

Meissner, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A;Accession: H84724

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-543 <STO>

C;Genetics:

A;Gene: At2g31770

A;Map position: 2

Query Match

Best Local Similarity 8.5%; Score 220; DB 2; Length 543;
Matches 60; Conservative 33; Mismatches 83; Indels 56; Gaps 11;

QY 235 NITCITCTDVRSPLVFOCNNSHIVLICDFEHLYCVRNLN---RQFHDPOGLSPC 289

Db 125 NIQGICCFSYTREBIAKVSCHPYCCTCWAGYITKIDPGCUCVKCPES 289

QY 290 VAGCPNSLKLHEFRIGEYQNYR-QQGAERCVLONGWVLCPRGGAGLL--PE 344

Db 179 SAAVGKOMIEDDTETKV-NKYSRSLTRLEVEGGKIKW---CPSSCGGAAVERGSE 232

QY 345 PDQKRYTCCEGGNGLGCFAFCRECKEAYHEG-ECSAVBEASGTTQAYRUDERAAQARW 403

Db 233 SSSYDVSLC-----CSYRFCCWNSEDADHSPPVQCDTV-----SKW 266

QY 404 -----EAAKRETIKTTCPCCRPHVPUVKNGGMMHKCPQPOQCRLEWCWNC 449

Db 267 IPKNODESENKNMLANSKPCPECKRPIBKNDQCNHMTCSAP-CGHFFCWMIC 317

RESULT 3

T00550 hypothetical protein KIAA0708 - human (fragment)

C;Species: *Homo sapiens* (man)

C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004

R;Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.

A;Title: Prediction of the coding sequences of unidentified human genes. X. The complete

A;Reference number: T00350

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Residues: 1-153 <ISH>

A;Cross-references: UNIPROT:Q8IWTF3; EMBL:AB014508; NID:93327229; PID:BA31683.1; PID:93

C;Genetics:

C;Experimental source: Brain

C;Note: KIAA0708

Query Match 8.5%; Score 219.5; DB 2; Length 1753;

Best Local Similarity 21.4%; Pred. No. 2.2e-08; Matches 125; Conservative 57; Mismatches 181; Indels 221; Gaps 32;

QY 1 MIVFVFRNSSHGFPEV--DSPTS-----IFOLK 27

Db 1012 MWLILKFQNOTEESVETULKSDSPELLLQMLVPLTSGNGPLTIEHGQDPFHGCVRLH 1071

QY 28 EVVAKRQG-----VPADQLRVIFACKELRNDRWTV-----QNCLDQQSI 66
Db 1072 EPGPDKSSGEALWLWLIPIPQAOYLNVERKDEGPTLEKANLISCLVRLKAHGKGKHLQ-L 1129

QY 67 VHIVQRPRWRKGQEMNATGDDPRAAGCEREPQLTRVPLSSVPGDSVGLAVLHID 126

Db 1130 VCLVLEAWOKGPNNPPTG----HTVAGGV---ACTSTDVLSCIL-HLIGQGV--- 1175

QY 127 SRKSPPP-----AGSPAGRSIYNSTFYVICKPVCORVQCKLKVQSTCROATLTQCP 180

Db 1176 KRRDRPDTLMVAPEFMGPGRQAOVPFCCSQSETSKPSPEAV-----ATLASLQP 1228

QY 181 SCMDVVLPNRMSGECOPHCPGTSAEFFRK--CGAHTSDKETPVAHILATNS--- 233

Db 1229 -----AGRMTSPO---EVEGLMKQTQVQEVTILEPDVQHQLAHSWGA 1272

QY 234 -----RNNTICITCDVRSV-----RNNTICITCDVRSV-----LVFOCNSRHVI 259

Db 1273 QLIQSYSEDPPEPLLAAGLCVHQAOAQAVPVRDPDHCPCV-----SPLGCDDLSLC-CMHYC 1328

QY 260 CLDCFHLYCVTRLNDRQFHDPOGLSYIC--VNGCP---NSLKEIHLHFRILGEBOYNR 314

Db 1329 CKSCMNEYLTTRI-----EONLVLNCCTPACPAQPTAFIRAI---VSPEVISK 1377

QY 315 YQQ-----XCAAECCVLOMGSVLPRLPRLP-GCGAGLILPEPDQRTCEGNGG---CGA 363

Db 1378 YEKALLRGY-VESC---SNLTWCTNPQCD-----RILCQGLGCGTCSKGWA 1423

QY 364 FCRECK-EAYHGECSAWEASGTTQAYRUDERAEQARW-----EASKE 409

Db 1424 SCFNCSFFEARHYPASC-----GHNMSQWUDGGYVGDGMSVEAQSKH 1463

QY 410 TIKKITKCCPCCRPHVPUVKNGGMMHKCPQPOQCRLEWCWNCGEW 453

Db 1464 LAUKISKRQSPCQAPILKNEGCLHMTC-AKCNHGFCHRLCKSW 1505

RESULT 4

T1477 hypothetical protein F56D2.5 - *Caenorhabditis elegans*

C;ID: 20-SEP-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

Db submitted to the EMBL Data Library, August 1994

A;Description: The sequence of *C. elegans* cosmid F56D2.

A;Reference number: Z15519

A;Accession: T1477

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-437 <DUZ>

A;Cross-references: UNIPROT:Q20871; EMBL:U1644; NID:9532100; PID:91945502; PID:AA85268-

A;Experimental source: strain Bristol N2; clone F56D2

A;Genetics: A;Gene: CESP_F56D2.5

A;Map position: 3

A;Introns: 41/3; 134/3; 185/3; 223/3; 254/2; 287/2; 414/3

QY 182 DSPTSFQKKEVVAKRGQVPAQDQIRVAGKEL--RUDWTWVNCDDQDQSIVHIVQRPR 75

Db 3 DRDLOIYEL-----BALESVIREKLUKASSDWSDNABE1-QGIEEV----- 42

QY 76 KGQEMNATGDDPRAAGCEREPQLTRVPLSSVPGDSVGLAVLHID 1175

Db 43 -----GFDNLVDPVTWTSDDSDQFHPLDLP-----PIRKFLPHLNDPYTVS 88

QY 136 SPAGRISIINSPYYVCKGSPCQRYQPGKLRVOSTCRATLITQGSCWMDVLLPRTMS 195

Run on: February 23, 2005, 13:25:39 ; Search time 102.258 seconds
 OM protein - protein search, using sw model

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GenCore version 5.1.6

Title: US-10-622-817-9

Perfect score: 2595

Sequence: I MIVFVRNSHGSFPPVENDS... CNGCCEWRVCMGDIWFDV 465

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_16sec04:*

1: geneseqP1990B:*

2: geneseqP2000B:*

3: geneseqP2001B:*

4: geneseqP2002B:*

5: geneseqP2003ab:*

6: geneseqP2003bb:*

7: geneseqP2004B:*

8: geneseqP2004B:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB	ID	Description
1	2596	100.0	465	2	AAY32501	Aay32501 Human par
2	2596	100.0	465	6	AAB330800	Aab330800 Human par
3	2596	100.0	465	6	AAB07156	Aab07156 Human par
4	2584	99.5	465	6	AAB330801	Aab330801 Human par
5	2405	92.6	437	2	AAY32502	Aay32502 Human par
6	2405	92.6	437	6	AAB07157	Aab07157 Human par
7	2170.5	83.6	464	4	AAB67517	Aab67517 Amino aci
8	2165.5	83.4	464	4	AAB67531	Aab67531 Amino aci
9	2165.5	83.4	464	4	AAB67532	Aab67532 Amino aci
10	2087.5	80.4	451	4	AAB67533	Aab67533 Amino aci
11	1696.5	65.4	316	6	AAB07158	Aab07158 Human p53
12	1679.5	64.7	344	4	AAB67521	Aab67521 Amino aci
13	1234.5	47.6	296	4	AAB67526	Aab67526 Amino aci
14	1058.5	40.8	468	4	AAB65114	Aab65114 Drosophili
15	1002	36.6	250	4	AAB67519	Aab67519 Amino aci
16	997	38.4	262	4	AAB67518	Aab67518 Amino aci
17	870	33.5	156	4	AAB67213	Aab67213 Amino aci
18	671.5	25.9	183	4	AAB67525	Aab67525 Amino aci
19	671.5	25.9	194	4	AAB67524	Aab67524 Amino aci
20	544.5	21.0	386	4	AAB86951	Aab86951 C. elegan
21	506	19.5	153	4	AAB67523	Aab67523 Amino aci
22	335	12.9	77	4	AAB67529	Aab67529 Amino aci
23	263	10.1	46	4	AAM17055	Aam17055 Peptide #
24	263	10.1	46	4	AAB36052	Aab36052 Peptide #
25	10.1	46	4		AAM29548	Aam29548 Peptide #

ALIGNMENTS

RESULT 1

ID AAY32501 standard; protein; 465 AA.

XX AAY32501;

XX DT 21-OCT-1999 (first entry)

XX DR Human parkin gene variant protein.

XX KW Parkinson's disease related gene; parkin gene; variant; gene therapy.

XX OS Homo sapiens.

XX PN WO940191-A1.

XX PD 12-AUG-1999.

XX PF 09-FEB-1999; 99NO-JP000545.

PR 09-FEB-1998; 980P-00027531.

XX PA (SHIMU/) SHIMIZU N.
 (MIZU/) MIZUNO Y.

XX PI Shimizu N, Mizuno Y;

XX DR WPI: 1999-494295/41.

DR N-PSDB; AAX9923.

XX PT Gene implicated in the pathology of Parkinson's disease, used for treatment of the disease.

XX PS Claim 1; Page 83-88; 114pp; English.

XX CC This sequence is encoded by a gene of the invention, and is implicated in the pathology of Parkinson's disease. This sequence is a variant of the parkin gene found in Parkinson's disease patients. The sequences may be used for the diagnosis, treatment (including gene therapy) and investigation of Parkinson's disease

CC Sequence 465 AA;

Query Match 100.0%; Score 2596; DB 2; Length 465;
 Best Local Similarity 100.0%; Pred. No. 2.3e-219;
 Matches 465; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIVFVRNSHGSFPPVENDSDTSIQLKERVAKRQGVPAQLRVIFAGKELRNDDWVNQCD 60

Db 1 MIVFVRFNSHGPFPVEVDSDISIFOLKEVAKRQGVADQLRVIPAGKELRNDFWQNCD
Qy 61 LDQOSIYHVTPWRKGQEMMAGGGDPRNAAGGEREPOSLTRVDLSSVLUGGDSVGLA 60
Db 61 LDQOSIYHVTPWRKGQEMMAGGGDPRNAAGGEREPOSLTRVDLSSVLUGGDSVGLA 120
Qy 121 VILHTPSRKDSPPGSPAGSPLRSIYNFSFYVKKGPCORVQPKLRYCOSTCRQATLTQGP 120
Db 121 VILHTPSRKDSPPGSPAGSPLRSIYNFSFYVKKGPCORVQPKLRYCOSTCRQATLTQGP 180
Qy 181 SCWDVLLPGRMSGEQSPPCGTSAEFFFKGAHPTSKETPVALTHIATNSRNITCIT 180
Db 181 SCWDVLLPGRMSGEQSPPCGTSAEFFFKGAHPTSKETPVALTHIATNSRNITCIT 240
Qy 241 CTDVASPVLYFQCMNSRHVICLDCFLHYCVTRLNDQFHDPOGLYSUFCVGCPNSLIKE 300
Db 241 CTDVASPVLYFQCMNSRHVICLDCFLHYCVTRLNDQFHDPOGLYSUFCVGCPNSLIKE 300
Qy 301 LHFRFLIGSEQNYRQYGAEECVLQMGVLCPRGCGAGLIREPDKRTCEGANGLG 360
Db 301 LHFRFLIGSEQNYRQYGAEECVLQMGVLCPRGCGAGLIREPDKRTCEGANGLG 360
Qy 361 GFAFCRECKEAYHEGCCSAVFEASGTTQAYRDERAEQAWEASKETIKTTKPCPR 420
Db 361 GFAFCRECKEAYHEGCCSAVFEASGTTQAYRDERAEQAWEASKETIKTTKPCPR 420
Qy 421 CHVVERKNGGMMHKCPQOQCRLEWCWNCGEGNWRVGMGDHFDV 465
Db 421 CHVVERKNGGMMHKCPQOQCRLEWCWNCGEGNWRVGMGDHFDV 465

RESULT 2

AAB30800
ID AAE30800 **standard; protein; 465 AA.**
XX
AC AAE30800;
XX
DT 24-FEB-2003 **(first entry)**
DE Human Parkin protein.
XX

KW Human; Parkin protein; neurological disorder; apoptosis; gene therapy; ischemic stroke; Parkinson's disease; Alzheimer's disease; neurologic; transgenic; cerebroprotective; neuroprotective; neurotransplantation. Homo sapiens.

FT Cleavage-site 126
PN WO20027945-A2.
XX
PD 10-OCT-2002.
XX
PF 02-APR-2002; 2002WO-DK000221.
XX
PR 29-MAR-2001; 2001DK-00000525.
PR 03-APR-2001; 2001US-0281286P.
XX
PA (NSGE-) NSGENE AS.
PI Jensen PH;
XX
DR WPI; 2003-046812/04.
DR N-PSDB; AND47679.
XX

PT New isolated nucleic acid sequence encoding a Parkin polypeptide, useful for treating, preventing or diagnosing neurological disorders, e.g. Parkinson's disease, Alzheimer's disease or ischemic stroke, and in screening assays.

XX

PS Claim 10; Page 69; 71pp; English.

RESULT 3

ABO07156
ID ABO07156 **standard; protein; 465 AA.**
XX
AC ABO07156;
XX
DT 13-AUG-2003 **(first entry)**
XX
DE Human p53 modifying protein, SEQ ID 116.
XX

KW Human; p53 modifier; cytostatic; cancer; cyrostatic; antiangiogenic; antiapoptotic; p53 patch; breast cancer; colon cancer; kidney cancer; lung cancer; ovarian cancer; angiogenesis; cell cycle; apoptotic disorder; cell proliferation disorder.

OS Homo sapiens.

PD	12-DEC-2002.	WO20020599122-A1.
XX	03-JUN-2002; 2002W0-US017382.	
PP		
XX		
PR	05-JUN-2001; 2001US-0296076P.	
PR	10-OCT-2001; 2001US-0328605P.	
PR	15-FEB-2002; 2002US-0357253P.	
XX		
PA	(EXBL-) EXELIXIS INC.	
XX		
PI	Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;	
DR	DR WPI; 2003-156859/15.	
XX	N-P5DB; ACDI3332.	
PT	Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53 pathway in <i>Drosophila</i> .	
XX		
PS	Example 2; Page 399-401; 67Bpp; English.	
XX		
CC	The invention relates to identifying (M1) a candidate p53 pathway modulating agent, by contacting an assay system comprising a purified HM polypeptide (human orthologue of genes that modify the p53 pathway in <i>Drosophila</i>) or nucleic acid with a test agent under conditions, where but for the presence of the test agent, the system provides a reference activity, and detecting a test agent-biased activity of the assay system. Also included are modulating (M2) a p53 pathway of a cell (comprising contacting a cell defective in p53 function with a candidate modulator that specifically binds to a HM polypeptide comprising an HM amino acid sequence, where p53 function is restored), modulating (M3) a p53 pathway in a mammalian cell (comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with a probe for HM expression; (c) comparing the results with a control; and (d) determining whether the comparison indicates a likelihood disease). (M1) is useful for identifying modulators of the p53 pathway. A probe for HM expression is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 % expression level. Modulators identified by (M1) are useful in a variety of diagnostic and therapeutic applications, where disease or disorder prognosis is related to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell proliferation disorders (e.g. cancer). Another two new methods (M2 and M3) are useful for modulating the p53 pathway of a cell, thus restoring the p53 function of the cell, so that the cell undergoes normal proliferation or progression through the cell cycle. (M2) and (M3) are also useful for treating defects in the p53 pathway such as angiogenic, apoptotic or cell proliferation disorders. The present sequence represents a human p53 pathway modifying protein	
CC	Sequence 465 AA;	
CC	Query Match 100.0%; Score 2596; DB 6; Length 465;	
CC	Best Local Similarity 100.0%; Pred. No. 2.3e-219; Matches 465; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
CC	Matches 465; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 MIVFRPNSSHGFPEVSDSTSIQFQKLEWKVAKRCQWPADOLRVIFAGKSELRLNDWTQNCQD 60	
DB	1 MIVFRPNSSHGFPEVSDSTSIQFQKLEWKVAKRCQWPADOLRVIFAGKSELRLNDWTQNCQD 60	
OY	61 LDQOSIVHTVORPKQGEMNATGGDDPRNAAGGEREPQLTRDLSSSVLPQSGVGLA 120	
DB	61 LDQOSIVHTVORPKQGEMNATGGDDPRNAAGGEREPQLTRDLSSSVLPQSGVGLA 120	
OY	121 VILHDSRKDSPPAGSPAGSIVNSYVWCKGCPGCRVQCGKQAHPTSDKETPVHLIATNSRNICIT 240	
DB	121 VILHDSRKDSPPAGSPAGSIVNSYVWCKGCPGCRVQCGKQAHPTSDKETPVHLIATNSRNICIT 240	
OY	181 SCWDPDVLLINRMMSGCQSPHCPCGTSAAFFKCGAHPTSDKETPVHLIATNSRNICIT 240	

Db	181	SCWDDDLIPNRMSGECQSPHCPGTSEFFPGCAGMTSDKTPVHALIATNSNITCT	240
Oy	241	CTDVRLRPLVLFQCNSHVTCDCFHLYCVTRLNDRQFVHDQCGSYLPVCAGCPNLSIKE	300
Db	241	CTDVRPLVLFQCNSHVTCDCFHLYCVTRLNDRQFVHDQCGSYLPVCAGCPNLSIKE	300
Qy	301	LHHFRILGEQYRNQYQGAECVQIQMGGVLCPRPGCAGLPEPDQRYTCESGGNGLC	360
Db	301	LHHFRILGEQYRNQYQGAECVQIQMGGVLCPRPGCAGLPEPDQRYTCESGGNGLC	360
Oy	361	GFAFCBCKEAYHEGCSAVFASGTTQAYRVEDRAAEQARWEASKEITKKTKPCR	420
Db	361	GFAFCBCKEAYHEGCSAVFASGTTQAYRVEDRAAEQARWEASKEITKKTKPCR	420
Oy	421	CHVPVKKGCGHMCKPQPOCRLEWGNNGCEWNWRVCMGDHWFDV	465
Db	421	CHVPVKKGCGHMCKPQPOCRLEWGNNGCEWNWRVCMGDHWFDV	465

AAE30801
 ID AAE30801 standard; protein; 465 AA.
 AAE30801;
 AC XX
 DT XX
 DE Human Parkin D126 mutant protein.
 KW Human; Parkin protein; neurological disorder; apoptosis; gene therapy;
 KW Ischemic stroke; Parkinson's disease; Alzheimer's disease; nootropic;
 KW trangenic; cerebroprotective; neuroprotective; neurotransplantation;
 KW mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 126 /note= "Wild-type Asp is replaced with Glu"
 FT Cleavage-site 126
 FT Misc-difference 223 /note= "Encoded by CCA"
 FT P02-APR-2002; 2002WO-DK000221.
 XX PR 29-MAR-2001; 2001DK-00000525.
 PR 03-APR-2001; 2001US-0281286P.
 XX PA (NSG3-) NSGENE AS.
 XX PI Jensen PH;
 XX DR WPI; 2003-046812/04.
 DR N-PSB; AAD47680.
 XX PT New isolated nucleic acid sequence encoding a Parkin polypeptide, useful
 PT for treating, preventing or diagnosing neurological disorders, e.g.
 PT Parkinson's disease, Alzheimer's disease or ischemic stroke, and in
 PT screening assays.
 XX
 PS Claim 10, Page 71, 71pp; English.

The invention relates to Parkin protein and its corresponding nucleic acid sequence. The nucleic acid sequence is useful for altering the proteolytic processing of Parkin at its potential cleavage site at Asp 126. The invention is used in manufacturing or testing a pharmaceutical composition for treating and/or preventing a neurological disorder, e.g.

CC Alzheimer's disease or ischaemic stroke. It also used for detecting the occurrence of proteolytic processing of Parkin at Asp 126 in a sample, in monitoring a potential disposition for a neurodegenerative disease, and for treating, preventing and/or diagnosing Parkinson's disease or other neurodegenerative disorders. The viral vector is used for transforming neuronal cells in vivo or ex vivo. The invention is useful for screening assays to identify compounds that increase or decrease neurotransplantation into the CNS of a mammal. It may be used in apoptosis. It is also used in gene therapy. The present sequence is human Parkin mutant protein.

SQ Sequence 465 AA;

Query Match 99.5%; Score 2584; DB 6; Length 465;
Best Local Similarity 99.6%; Pred. No. 2.6e-218; Matches 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTIVFVRFNSHGPFPVEVDSDTSIFOLKEVAKRQGYPADQRVTFAGKELRNDDWVNQCD 60

Db 1 MTIVFVRFNSHGPFPVEVDSDTSIFOLKEVAKRQGYPADQRVTFAGKELRNDDWVNQCD 60

QY 61 LDQOSIVHIVQRPWRKGQEMNATGGDPDPRNAAGGEREPOSILTRDLSVSLPDSVGLA 120

Db 61 LDQOSIVHIVQRPWRKGQEMNATGGDPDPRNAAGGEREPOSILTRDLSVSLPDSVGLA 120

QY 121 VILHTRSRKDSPPSPAGSPGRSISYNSFYVCKGKPCORVQPKLRLVQCGTSCROATLTQGP 180

Db 121 VILHTRSRKDSPPSPAGSPGRSISYNSFYVCKGKPCORVQPKLRLVQCGTSCROATLTQGP 180

QY 181 SCWDDVLIPNRMGSGCOSPIRGPSAEEFKCGAHPSTSKEPVALTHIATNSRNITCT 240

Db 181 SCWDDVLIPNRMGSGCOSPIRGPSAEEFKCGAHPSTSKEPVALTHIATNSRNITCT 240

QY 241 CTDVSPSPVLFQCNRSRIVCUDCFHYCVTRLNDRQFDHPDOLGYSLPCVAGCPNSLIKE 300

Db 241 CTDVSPSPVLFQCNRSRIVCUDCFHYCVTRLNDRQFDHPDOLGYSLPCVAGCPNSLIKE 300

QY 301 LHHRFLIGEQINRYQQYGAECVCLQMGAVLCPRGCGAGLALPEPDORKVTCRGGNLGC 360

Db 301 LHHRFLIGEQINRYQQYGAECVCLQMGAVLCPRGCGAGLALPEPDORKVTCRGGNLGC 360

QY 361 GFAFCRECKEAYHGGCSAVFEASGTTOQAYRVDERAQWEASKETIKTTKPCPR 420

Db 361 GFAFCRECKEAYHGGCSAVFEASGTTOQAYRVDERAQWEASKETIKTTKPCPR 420

QY 421 CHVVEKNGGCMANKKCPQPOCRLEWCWNCGCWNRVCMGDHWFDV 465

Db 421 CHVVEKNGGCMANKKCPQPOCRLEWCWNCGCWNRVCMGDHWFDV 465

RESULT 5
AAV32502

ID AAV32502 standard; protein; 437 AA.

AC AAV32502;

DE 21-OCT-1999 (first entry)

XX Human parkin gene variant protein.

KW Parkinson's disease related gene; Parkin gene; variant; gene therapy.
XX Homo sapiens.

OS Homo sapiens.

XX WO9940191-A1.

PN 12-AUG-1999.

PD 09-FEB-1999; 99WO-JP000545.

PR 09-FEB-1998; 98JP-0027531.

PA (SHIMIZU) SHIMIZU N.

PA (MIZU/) MIZUNO Y.
XX Shimizu N., Mizuno Y;
FI XX
DR XX WPI; 1999-493295/41.
XX DR-N-PSDB; AAX39924.

PT Gene implicated in the pathology of Parkinson's disease, used for
XX treatment of the disease.

PS Claim 1; Page 89-94; 114pp; English.

XX This sequence is encoded by a gene of the invention, and is implicated in
CC the pathology of Parkinson's disease. This sequence is a variant of the
CC parkin gene found in parkinson's disease patients. The sequences may be
CC used for the diagnosis, treatment (including gene therapy) and
CC investigation of Parkinson's disease.

SQ Sequence 437 AA;

Query Match 92.6%; Score 2405; DB 2; Length 437;
Best Local Similarity 94.0%; Pred. No. 1.3e-202; Matches 437; Mismatches 0; Indels 28; Gaps 1;

QY 1 MTIVFVRFNSHGPFPVEVDSDTSIFOLKEVAKRQGYPADQRVTFAGKELRNDDWVNQCD 60

Db 1 MTIVFVRFNSHGPFPVEVDSDTSIFOLKEVAKRQGYPADQRVTFAGKELRNDDWVNQCD 60

QY 61 LDQOSIVHIVQRPWRKGQEMNATGGDPDPRNAAGGEREPOSILTRDLSVSLPDSVGLA 120

Db 61 LDQOSIVHIVQRPWRKGQEMNATGGDPDPRNAAGGEREPOSILTRDLSVSLPDSVGLA 120

QY 61 LHHRFLIGEQINRYQQYGAECVCLQMGAVLCPRGCGAGLALPEPDORKVTCRGGNLGC 360

Db 61 LHHRFLIGEQINRYQQYGAECVCLQMGAVLCPRGCGAGLALPEPDORKVTCRGGNLGC 360

QY 121 VILHTRSRKDSPPSPAGSPGRSISYNSFYVCKGKPCORVQPKLRLVQCGTSCROATLTQGP 180

Db 121 VILHTRSRKDSPPSPAGSPGRSISYNSFYVCKGKPCORVQPKLRLVQCGTSCROATLTQGP 180

QY 181 SCWDDVLIPNRMGSGCOSPIRGPSAEEFKCGAHPSTSKEPVALTHIATNSRNITCT 240

Db 181 SCWDDVLIPNRMGSGCOSPIRGPSAEEFKCGAHPSTSKEPVALTHIATNSRNITCT 240

QY 241 CTDVSPSPVLFQCNRSRIVCUDCFHYCVTRLNDRQFDHPDOLGYSLPCVAGCPNSLIKE 300

Db 241 CTDVSPSPVLFQCNRSRIVCUDCFHYCVTRLNDRQFDHPDOLGYSLPCVAGCPNSLIKE 300

QY 301 LHHRFLIGEQINRYQQYGAECVCLQMGAVLCPRGCGAGLALPEPDORKVTCRGGNLGC 360

Db 301 LHHRFLIGEQINRYQQYGAECVCLQMGAVLCPRGCGAGLALPEPDORKVTCRGGNLGC 360

QY 361 GFAFCRECKEAYHGGCSAVFEASGTTOQAYRVDERAQWEASKETIKTTKPCPR 420

Db 361 GFAFCRECKEAYHGGCSAVFEASGTTOQAYRVDERAQWEASKETIKTTKPCPR 420

QY 421 CHVVEKNGGCMANKKCPQPOCRLEWCWNCGCWNRVCMGDHWFDV 465

Db 421 CHVVEKNGGCMANKKCPQPOCRLEWCWNCGCWNRVCMGDHWFDV 465

RESULT 6
ABO07157

ID ABO07157 standard; protein; 437 AA.

AC ABO07157;

XX 13-AUG-2003 (first entry)

XX Human p53 modifying protein, SEQ ID 117.

DE XX

XX Human p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;

XX antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;

XX lung cancer; ovarian cancer; angiogenesis; cell cycle;

XX apoptotic disorder; cell proliferation disorder.

OS Homo sapiens.

SQ	Sequence 464 AA;	PT	a transgenic non-human animal as an animal model for neurodegenerative diseases.
Query Match	83.6%; Score 2170.5; DB 4; Length 464;	PT	
Best Local Similarity	83.4%; Pred. No. 6e-182;	XX	
Matches	388; Conservative 29; Mismatches 47; Indels 1; Gaps 1;	PS	Claim 7; Page 47-49; 62pp; English.
QY	1 MIVFVRFNSHSGPVEVDSDTSIFOLKEVAKRQGPADQRVTFAGKELRNDWTVQCD	CC	The present sequence represents a murine parkin2 polypeptide. The sequence contains the mutation Lys61Asn. Mutations or deletions in the parkin2 gene cause Parkinson's disease in humans. The human parkin2 gene is located in gene region q925.2-27. Parkin2 polypeptides and polynucleotides are useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, Multi-system atrophy, Wilson's disease, Pick's disease, Prion disease, and secondary causes inducing Parkinson's syndromes like toxins, drugs, brain tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated with a less active or non-active parkin protein.
Db	1 MIVFVRFNSHSGPVEVDSDTSIFOLKEVAKRQGPADQRVTFAGKELRNDWTVQCD	CC	
QY	61 LDQSQIYHIVTPRPARQGQMNATGGDPDPRNAAGCEREPPOSTSITRVDLSSSVLPGDSVGLA	CC	
Db	61 LDQSQIYHIVTPRPARQGQMNATGGDPDPRNAAGCEREPPOSTSITRVDLSSSVLPGDSVGLA	CC	
QY	61 LDQSQIYHIVTPRPARQGQMNATGGDPDPRNAAGCEREPPOSTSITRVDLSSSVLPGDSVGLA	CC	
Db	61 LDQSQIYHIVTPRPARQGQMNATGGDPDPRNAAGCEREPPOSTSITRVDLSSSVLPGDSVGLA	CC	
QY	181 SCWDDVLINPMSGECQSPHPGTAEFFKCGAMPSTSKEPTVPHIATSNRNTCTT 240	CC	
Db	180 SCWDDVLINPMSGECQSPHPGTAEFFKCGAMPSTSKEPTVPHIATSNRNTCTT 240	CC	
QY	241 CTDVSPSPVLFQCNRSRHYICIDCPFLYCVTRLNDRQFVHDPLQGYSLPCVAGCPNSLIKE	CC	
Db	240 CTDVSPSPVLFQCNRSRHYICIDCPFLYCVTRLNDRQFVHDPLQGYSLPCVAGCPNSLIKE	CC	
QY	301 LHHRFLIGEQQYNRQYQGAECVLUQMGGLCPRPQGAGLGLPEPDORKTVTEGGNGLGC	360	
Db	300 LHHRFLIGEQQYNRQYQGAECVLUQMGGLCPRPQGAGLGLPEPDORKTVTEGGNGLGC	359	
QY	361 GFAFCRECKEAHIEGECSAVFASGTTQAVDERAQARWEASKETIKKTKPCPR 420	419	
Db	360 GFVFRCRDCKEAYHSGDCDSLLEPSGATSOAQRUDKRAAEQARWEASKETIKKTKPCPR	419	
QY	421 CHVPVEKGGMEMMKCQPOQCRLEWCWNCGCEBNRVCMDHWFDV 465		
Db	420 CNVPIEKNGGCMIMMKCQPOQCRLEWCWNCGCEBNRVCMDHWFDV 464		
RESULT 8		PT	
AAB67531		PT	
ID AAB67531	standard; protein; 464 AA.	XX	
AC AAB67531;		PS	
XX		XX	
DT 29-MAY-2001	(first entry)	XX	
DE Amino acid sequence of a mutated murine parkin2 polypeptide.		XX	
KW	Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease;	XX	
KW	Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis;	XX	
KW	Mult-system atrophy; Wilson's disease; Pick's disease; Prion disease;	XX	
KW	brain tumour; head trauma; stroke; vascular irregularity;	XX	
KW	metabolic irregularity.	XX	
OS Mus sp.		XX	
XX		XX	
EN EPI081225-A1.		XX	
PD 07-MAR-2001.		XX	
PP 30-AUG-1999; 99EP-00116766.		XX	
PR 30-AUG-1999; 99EP-00116766.		XX	
PA (BIOF-) BIOPRONTIERA PHARM GMBH.		XX	
XX		XX	
PT Duebbert H;		XX	
XX		XX	
WPI; 2001-212797/22.		XX	
NN-PSDB; RAFF5258.		XX	
, PT New polynucleotides encoding mouse parkin2 protein, useful for producing		XX	
RESULT 9		PT	
AAB67532		PT	
ID AAB67532	standard; protein; 464 AA.	XX	
AC AAB67532;		XX	
XX		XX	
DT 29-MAY-2001	(first entry)	XX	
DE Amino acid sequence of a mutated murine parkin2 polypeptide.		XX	
KW	Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease;	XX	
KW	Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis;	XX	
KW	Mult-system atrophy; Wilson's disease; Pick's disease; Prion disease;	XX	
KW	brain tumour; head trauma; stroke; vascular irregularity;	XX	
KW	metabolic irregularity.	XX	

XX	OS	Mug BP.
PN	XX	EP1081225-A1.
XX	XX	RESULT 10
PD	ID	AAB67533
XX	AC	AAB67533 standard; protein; 451 AA.
PF	XK	AAB67533;
XX	AC	AAB67533;
PR	XX	AAB67533;
XX	DT	29-MAY-2001 (first entry)
PA	XX	
(BIOF-) BIOFRONTERA PHARM GMBH.	DE	Amino acid sequence of a mutated murine parkin2 polypeptide.
XX	XX	
PI	KW	Parkin2; Parkinson's disease; 6925-2-27; neurodegenerative disease;
Luebbert H;	KW	Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis;
XX	KW	Multi-system atrophy; Wilson's disease; Pick's disease; Prion disease;
DR	KW	brain tumour; head trauma; stroke; vascular irregularity;
N-PSDB; AAF55259.	KW	metabolic irregularity.
PT	OS	
PT	OS	New polynucleotides encoding mouse parkin2 protein, useful for producing
PT	OS	a transgenic non-human animal as an animal model for neurodegenerative
PT	OS	diseases.
XX	OS	
PS	OS	Claim 7; Page 49-51; 62pp; English.
XX	OS	
CC	XX	The present sequence represents a murine parkin2 polypeptide. The
CC	XX	sequence contains the mutation Thr415Asn. Mutations or deletions in the
CC	XX	parkin2 gene cause Parkinson's disease in humans. The human parkin2 gene
CC	XX	is located in gene region 6925-2-27. Parkin2 polyPeptides and
CC	XX	polynucleotides are useful for testing the efficacy of the treatment of a
CC	XX	neurodegenerative disease such as Parkinson's disease, Alzheimer's
CC	XX	disease, Huntington's disease, amyotrophic lateral sclerosis, Multi-
CC	XX	system atrophy, Wilson's disease, Pick's disease, Prion disease, and
CC	XX	secondary causes inducing Parkinson's syndromes like toxins, drugs, brain
CC	XX	tumours, head trauma, stroke, vascular irregularities or metabolic
CC	XX	irregularities, associated with a less active or non-active parkin
CC	XX	protein
SQ	XX	
Sequence 464 AA:	XX	
Query Match	83.4%	Score 2165.5; DB 4; Length 464;
Best Local Similarity	83.2%	Pred. No. 1.7e-181; Indels 1; Gaps 1;
Matches	387; Conservative	Mismatches 29; Mismatches 48;
Qy	1	MIVFVRPNSSHGPPVEVSDTSIFOLKEVAKRQGVPAQDQLRVTAGKEVLNDWTVNQCD 60
Db	1	MIVFVRPNSSHGPPVEVSDTSIFOLKEVAKRQGVPAQDQLRVTAGKEVLNDWTVNQCD 60
Qy	61	LDQSQSIVHVQRPWKGQEMNATGGDDPRAAGGGEREPOSLTRVLDLSSAVLPGSVGLA 120
Db	61	LEQQSIVHVQRPWRSHTHMASGDEPOSTSEGSIWESELSTRYRDLSSHTLPVDSVGLA 120
Qy	121	VLIHTDSRKSPPPAGSPAGHSIVNSPYVWCCKGPCCRQVQPLRVCSTCROATLTQGP 180
Db	121	VLIHTDSRKSPPPAGSPAGHSIVNSPYVWCCKGPCCRQVQPLRVCSTCROATLTQGP 180
Qy	121	VLIHTDSRKSPPPAGSPAGHSIVNSPYVWCCKGPCCRQVQPLRVCSTCROATLTQGP 179
Db	181	SCWDDVLIPNRMSCGCQSPHCPGTSAEFFKGAAHTPSDKETPVIAHLATNSRNITCIR 240
Qy	180	SCWDDVLIPNRMSCGCQSPHCPGTRAEFFFKGAAHTPSDKTSVALNLITNSRNISPCIA 239
Db	241	CTDVRSPLVLFQCNRSRHVICDCEFLYCVTRLNDRQFVHPDQLGSLIPCVAGCPNSLIKE 300
Qy	240	CTDVRSPLVLFQCNRSRHVICDCEFLYCVTRLNDRQFVHPDQLGSLIPCVAGCPNSLIKE 299
Db	301	LHHFRFLRGEBYQNYQQGABECVQMGGYLCPRGCGACILPERDQKRTCEGNGLGC 360
Db	300	LHHFRFLRGEBYQTRIQQYGAEECIVQMGGLCPRGCGACILPERDQKRTCEGNGLGC 359
Qy	361	GFAFRECKEAYHSECASAVEASCTTQYVDPBRAASCARWENASKETIKTKTPCPR 420
Db	360	GFVFRDCKEAYHEDCDSSLERSCATSQRVDRKRAEOARWEBASKETIKTKTPCPR 419
Qy	421	CHVIVEKNGCMHMKCPQPCRLECWNCCEWMVCMDHWDV 465
Qy	XX	
Sequence 451 AA:	XX	
Query Match	80.4%	Score 2087.5; DB 4; Length 451;
Best Local Similarity	83.2%	Pred. No. 1.2e-174; Indels 1; Gaps 1;
Matches	376; Conservative	Mismatches 29; Mismatches 46;
Qy	1	MIVFVRPNSSHGPPVEVSDTSIFOLKEVAKRQGVPAQDQLRVTAGKEVLNDWTVNQCD 60
Db	1	MIVFVRPNSSHGPPVEVSDTSIFOLKEVAKRQGVPAQDQLRVTAGKEVLNDWTVNQCD 60
Qy	61	LDQSQSIVHVQRPWKGQEMNATGGDDPRAAGGGEREPOSLTRVLDLSSAVLPGSVGLA 120
Db	61	LEQQSIVHVQRPWRSHTHMASGDEPOSTSEGSIWESELSTRYRDLSSHTLPVDSVGLA 120
Qy	121	VLIHTDSRKSPPPAGSPAGHSIVNSPYVWCCKGPCCRQVQPLRVCSTCROATLTQGP 180

sequence, where p53 function is restored), modulating (M3) a p53 pathway in a mammalian cell (comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with a probe for HM expression; (c) comparing the results with a control; and (d) determining whether the comparison indicates a likelihood disease). (M1) is useful for identifying modulators of the p53 pathway. A probe for HM expression is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25% expression level. Modulators identified by (M1) are useful in a variety of diagnostic and therapeutic applications, where disease or disorder prognosis is related to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell proliferation disorders (e.g. cancer). Another two new methods (M2 and M3) are useful for modulating the p53 pathway of a cell, thus restoring the p53 function of the cell, so that the cell undergoes normal proliferation or progression through the cell cycle. (M2) and (M3) are also useful for treating defects in the p53 pathway such as angiogenic, apoptotic or cell proliferation disorders. The present sequence represents a human p53 pathway modifying protein.

KW brain tumour; head trauma; stroke; vascular irregularity;
 KW metabolic irregularity.
 XX :|||:|||:|||:|||:
 OS Mus sp.
 PN EP1081225-A1.
 XX PD 07-MAR-2001.
 XX PP 30-AUG-1999; 99EP-00116766.
 XX PR 30-AUG-1999; 99EP-00116766.
 XX PA (BIOF-) BIOFRONTERA PHARM GMBH.
 XX PI Luebbert H;
 XX DR WPI; 2001-212797/22.
 XX N-PSDB; AAFF55248.
 PT New polynucleotides encoding mouse parkin2 protein, useful for producing
 PT a transgenic non-human animal as an animal model for neurodegenerative
 PT diseases.
 XX PS Claim 7; Page 40-41; 62pp; English.
 XX CC The present sequence represents a murine parkin2 polypeptide. The
 CC polynucleotide sequence contains a deletion, leading to a truncated
 CC protein. Mutations or deletions in the parkin2 gene cause Parkinson's
 CC disease in humans. The human parkin2 gene is located in gene region
 CC 6q25.2-27. Parkin2 polypeptides and polynucleotides are useful for
 CC analysing neurodegenerative diseases. They are also useful for testing
 CC the efficacy of the treatment of a neurodegenerative disease such as
 CC Parkinson's disease, Alzheimer's disease, Huntington's disease,
 CC amyotrophic lateral sclerosis, Multi-system atrophy, Wilson's disease,
 CC Pick's disease, Prion disease, and secondary causes inducing Parkinson's
 CC syndromes like toxins, drugs, brain tumours, head trauma, stroke,
 CC vascular irregularities or metabolic irregularities, associated with a
 CC less active or non-active parkin protein
 XX SQ Sequence 344 AA:
 Query Match 64.7%; Score 1679.5; DB 4; Length: 344;
 Best Local Similarity 66.0%; Pred. No. 6.3e-139;
 Matches 307; Conservative 14; Mismatches 23; Indels 121; Gaps 1;
 PR 1 MIVFVRPNSSHGFPVVEDSDTSIFOLKEVAKRQGVPAQDLRVIPIAGKELRNDDWTQNCD 60
 DB |||||||:|||:|||:|||:|||:|||:
 1 MIVFVRPNSSHGFPVVEDSDTSIFOLKEVAKRQGVPAQDLRVIPIAGKELRNDDWTQNCD 60
 CC 61 LDQOSTIVHIVORPWRKGQEMMATTGQDPRNAAGGCEREPLOSSITRVDLSSVTPGSVGLA 120
 CC 57 ---
 CC 121 VLIHTDSRKSPGSPAGSTYNSPVYVCKPCQRVQPGKURVQCSTCROATLITQGP 180
 CC 57 ---
 CC 181 SCWDDVLIPNRMGECOSPHCEGTSABFFKGAHTSDKEPVIAHLIATNSRNITC 240
 DB 60 SCWDDVLIPNRMGECOSPHCEGTSABFFKGAHTSDKEPVIAHLIATNSRNITC 119
 CC 241 CTDVRSPLVUFOCNSRHIVTCDCFLHYCVTRNDROFVHDPOGLYSLPCVAGCPNSLIKE 300
 DB 120 CTDVRSPLVUFOCNSRHIVTCDCFLHYCVTRNDROFVHDPOGLYSLPCVAGCPNSLIKE 179
 CC 301 LHFRFLIGERQNYQYGAECVUQMGVLPCCGGAGLREPCKRKTCGEGNGLG 360
 DB 180 LHFRFLIGERQNYQYGAECVUQMGVLPCCGGAGLREPCKRKTCGEGNGLG 239
 CC 361 GFAFCRCKEAYHEGECSAVEEASGTTQAVYDNERAARQARWEASKETIKTKPCP 420
 DB 240 GFVFRCRCKEAYHEGOODSLEUPSGATSQAVYDNERAARQARWEASKETIKTKPCP 299

QY 421 CHVPUVKNGGHHMKCOPQQCLEWNCVCGEWRVCMGDHWPDV 465
 QY :|||:|||:|||:|||:
 Db 300 CNVPIEKNGGHHMKCOPQQCLEWNCVCGEWRVCMGDHWPDV 344

RESULT 13
 AAB67526
 ID AAB67526 standard; protein; 296 AA.
 XX DE Amino acid sequence of a murine truncated parkin2 polypeptide.
 XX AC AAB67526;
 XX DT 29-MAY-2001 (first entry)
 XX DE Amino acid sequence of a murine truncated parkin2 polypeptide.
 XX PR Parkin2; Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis;
 KW Alzheimer's disease; Wilson's disease; Pick's disease; Prion disease;
 KW Multi-system atrophy; brain tumour; head trauma; stroke; vascular irregularity;
 KW metabolic irregularity.
 XX OS Mus sp.

PN EP1081225-A1.
 XX PD 07-MAR-2001.
 XX PF 30-AUG-1999; 99EP-00116766.
 PR 30-AUG-1999; 99EP-00116766.
 PA (BIOF-) BIOFRONTERA PHARM GMBH.
 XX PI Luebbert H;
 XX DR WPI; 2001-212797/22.
 XX N-PSDB; AAFF55253.
 PT New polynucleotides encoding mouse parkin2 protein, useful for producing
 PT a transgenic non-human animal as an animal model for neurodegenerative
 PT diseases.
 XX PS Claim 7; Page 44-45; 62pp; English.
 XX CC The present sequence represents a murine parkin2 polypeptide. The
 CC polynucleotide sequence contains a deletion, leading to a truncated
 CC protein. Mutations or deletions in the parkin2 gene cause Parkinson's
 CC disease in humans. The human parkin2 gene is located in gene region
 CC 6q25.2-27. Parkin2 polypeptides and polynucleotides are useful for
 CC analysing neurodegenerative diseases. They are also useful for testing
 CC the efficacy of the treatment of a neurodegenerative disease such as
 CC Parkinson's disease, Alzheimer's disease, Huntington's disease,
 CC amyotrophic lateral sclerosis, Multi-system atrophy, Wilson's disease,
 CC Pick's disease, Prion disease, and secondary causes inducing Parkinson's
 CC syndromes like toxins, drugs, brain tumours, head trauma, stroke,
 CC vascular irregularities or metabolic irregularities, associated with a
 CC less active or non-active parkin protein
 XX SQ Sequence 296 AA:
 Query Match 47.6%; Score 1234.5; DB 4; Length 296;
 Best Local Similarity 80.0%; Pred. No. 7.3e-100;
 Matches 232; Conservative 20; Mismatches 37; Indels 1; Gaps 1;
 PR 1 MIVFVRPNSSHGFPVVEDSDTSIFOLKEVAKRQGVPAQDLRVIPIAGKELRNDDWTQNCD 60
 DB 1 MIVFVRPNSSHGFPVVEDSDTSIFOLKEVAKRQGVPAQDLRVIPIAGKELRNDDWTQNCD 60
 QY 61 LDQOSTIVHIVORPWRKGQEMMATTGQDPRNAAGGCEREPLOSSITRVDLSSVTPGSVGLA 120
 DB 61 LDQOSTIVHIVORPWRKGQEMMATTGQDPRNAAGGCEREPLOSSITRVDLSSVTPGSVGLA 120

QY 121 VILMDRSRDKSPPGSPAGRSIYNSFYVYCKGCQRYQPKLKVQCSCTCROATLTQGP 180
Db 121 VILMDRSRDKSPPGSPAGRSIYNSFYVYCKGCQRYQPKLKVQCSCTCROATLTQGP 179
QY 181 SCMDVLINRMSSGECQSPHCPGTSAAFFKCGAHTSDKETPVALHIAITMSRNITCIT 240
Db 180 SCMDVLINRMSSGECQSPHCPGTSAAFFKCGAHTSDKETPVALHIAITMSRNITCIT 239
QY 241 CTDVRSPVLAFCQNSRHRVHICLDCMHLYCVTRLANDQFVHDPOLGYSLPCV 290
Db 240 CTDVRSPVLAFCQNSRHRVHICLDCMHLYCVTRLANDQFVHDPOLGYSLPCV 289
RESULT 14

ABB65114 ABB65114 standard; protein; 468 AA.
XX AC ABB65114;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 22134.
XX KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
XX OS Drosophila melanogaster.
PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PR 23-MAR-2001; 2001WO-US009231.
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX PA (PEKE) PE CORP NY.
XX PT Venter JC, Adams M, Li PWD, Myers EW;
XX DR WPI; 2001-6556860/75.
XX DR N-PSDB; ABB69217.
XX PS Disclosure: SEQ ID NO 22134; 21pp + Sequence Listing; English.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
XX PR Disclosure: SEQ ID NO 22134; 21pp + Sequence Listing; English.
CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB5777-CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB5777-CC ABB7027). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 468 AA;

Query Match 40.8%; Score 1059.5; DB 4; Length 468;
Best Local Similarity 42.6%; Pred. No. 4e-84;
Matches 201; Conservative 80; Mismatches 158; Indels 33; Gaps 9;

QY 3 VFVRNFSHGFPPVEVSDTSIFOLKEVKVAKHQVPAQDOLRVIFACKELRNDWVNCIDP 62
Db 18 IYVKINTKGKTLTIVNLBQPWNLIKVNKLVAQGLQDDKIKIFAGKELSDATTIEQCIDG 77
QY 63 QOSIVHQ-RPWRKGQEMMAGGGDPRNAGGCRRPSSLTVLSSSLVPLPSDVGAV 121

Db 78 QOSVHLAIRLRLPPVQRQKIQSATLEEEPEPSLDEASKPMLNETLIDLQ----- 124
QY 122 ILHTDSRKDSPPGSFAGRSIYNSFYVYCKGCQRYQPKLKVQCSCTCROATLTQGS 181
Db 125 -LESEERLNITDVERVRAKA--HFFVHC-SOCDKLCLNGKURVCALCKGAGFTVHRDPE 179
QY 182 CWDVDLIPNRMSSGECQSPHCPGTS---AEPFKCGAHT-SDKETPVALHIAITMSRNITCIT 232
Db 180 CWDVDLIPNRMSSGECQSPHCPGTS---AEPFKCGAHT-SDKETPVALHIAITMSRNITCIT 239
QY 233 SRNITCITCIVRSPLVFOCNSRHWICLDCPHLYCVTRLANDQFVHDPOLGYSLPCV 292
Db 240 IKNVPLACITDVSDTLVFFCASORVTCDFRHYCRSLRGERQMPHDFGYILPCAG 299
QY 293 CPNSLITKELHFRIGEENFNYQGAECVLPQMGVNPQRCGAGILPEPQKRYC 352
Db 300 CEHSFTEEHFKLLTREYDRYORFATSVYVQKGGVCPQPGGMGLIVEPDKRKYC 359
QY 353 EGGNGLGGCAFRCRECKAYHEGEC-SAWFEASGTTQIYRVDRAEQAORWEASKETI 411
Db 360 QN---GCGYVFCRNLYGTHIGCGLPBTGASATNTSCYTVDNRRAEARWABASNTI 415
QY 412 KRTTKPCPCHRHPVPTKNG3EMHMKCPQPOCRLEWCWNCCCEWWNRCVMGRHWF 463
Db 416 KVSTKPCPKCRIPTERDGSGMMHVCTRAGCGFPENCWVCOTEWTRDCMGAIWF 467
RESULT 15

ABB67519 ABB67519 standard; protein; 250 AA.
XX AC ABB67519;
XX DT 29-MAY-2001 (first entry)
XX DE Amino acid sequence of a murine parkin2 polypeptide.
XX KW Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease; Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis; Multi-system atrophy; Wilson's disease; Pick's disease; Prion disease; brain tumour; head trauma; stroke; vascular irregularity; metabolic irregularity.
XX OS Mus sp.
XX PN EP1081225-A1.
XX PD 07-MAR-2001.
XX PR 30-AUG-1999; 99EP-00116766.
XX PR 30-AUG-1999; 99EP-00116766.
XX PA (BIOF-) BIOFRONTERA PHARM GMBH.
XX PT Luebbert H;
XX DR WPI; 2001-212797/22.
DR N-PSDB; AAF5246.
XX PT New polynucleotides encoding mouse parkin2 protein, useful for producing a transgenic non-human animal as an animal model for neurodegenerative diseases.
XX PS Claim 7; Page 21-22; 62pp; English.
XX The present sequence represents a murine parkin2 polypeptide. Mutations or deletions in the parkin2 gene cause Parkinson's disease in humans. The human Parkin2 gene is located in gene region 6q25.2-27. Parkin2 polypeptides and polynucleotides are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral

CC sclerosis, Multi-system atrophy, Wilson's disease, Prion
 CC disease, and secondary causes inducing Parkinson's syndromes like toxins,
 CC drugs, brain tumours, head trauma, stroke, vascular irregularities or
 CC metabolic irregularities, associated with a less active or non-active
 XX parkin protein

SQ sequence 250 AA;

Query Match 38.6%; Score 1002; DB 4; Length 250;
 Best Local Similarity 77.6%; Pred. No. 1; e-79; Matches 190; Conservative 20; Mismatches 35; Indels 0; Gaps 0;

Qy	1	MIVFVERNSIGGPPVVEDSDPISIQLKEVWAKRQGPADQAVIFAGKELURNDWTQNCD	60
	1	MIVFVRPNSSYGPVEVSDTSIQLKEVAKRQGVPAODQAVIFAGKELPNHLATVONCD	60
Qy	61	LDDQSVIHWIVOPWRKGQEMMNTGGDPRNAGGERBPOSLTRVDSLSSVLPGSVGLA	120
	61	LEQQSVIHWIVOPPRRSHETNASGGBPQSTSEGSIWESRLITRVQLSHTRPVNSVGLA	120
Db	121	VILHTPSRKDSPPAGSPAGRSIYNSPVYCKGPQRCVQPGKLRVQSTCROATLTHQGP	180
Qy	121	VILDTSKRSKDSBARGPAVKCTYNSFPFYICKGPCKHVQPGKLRLVQCGTCKORTLIAQGP	180
Db	181	SCWDDVLIPMSGECOSPHCPGTSAEFFKIGAHPSTSKETPVALHLATMSRNVCIT	240
Qy	181	SCWDDVLIPNRMSGECOSPDCEGTRAFFPKKGAAHPTSDKOTSVALNLITSNRRSIPCA	240
Qy	241	CTDVR 245	
Db	241	CTDVR 245	

Search completed: February 23, 2005, 13:50:13
 Job time : 103.258 secs

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Db 361 GFAFCRECKEAYHEGCSAVFASGTTQAYRDRAAEQRWEASKETIKKTKPCR 420 ; Patent No. 6716621
 Qy 421 CHVPEVKNGGCMHMKCPOPOCRLEWCNWCNGCEMNVRVCGMDHFDV 465 ; GENERAL INFORMATION:
 Db 421 CHVPEVKNGGCMHMKCPOPOCRLEWCNWCNGCEMNVRVCGMDHFDV 465 ; APPLICANT: Shimizu, No. 6716621uyoshi
 ; FILE REFERENCE: 065_2110000
 ; CURRENT APPLICATION NUMBER: US/09/601,844B
 ; PRIOR APPLICATION NUMBER: PCT/JP99/00545
 ; PRIOR FILING DATE: 1999-02-09
 ; NUMBER OF SEQ ID NOS: 70
 ; SEQ ID NO: 4
 ; SOFTWARE: Patentin version 3.1
 ; LENGTH: 437
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-601-844B-4

Query Match 100.0%; Score 2596; DB 4; Length 465;
 Best Local Similarity 100.0%; Pred. No. 8_4e-251; Matches 465; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MIVFVRNSHGPVVEUDSDTSIFOLKEVAKRQGVPAQDRLVITAGKEURNDWVQCD 60 ;
 Db 1 MIVFVRNSHGPVVEUDSDTSIFOLKEVAKRQGVPAQDRLVITAGKEURNDWVQCD 60 ;
 Qy 61 LDQOSIVHIVQRPWKQEMNATGGDPRAAGGEREPOLSTTRVDLSSVLPGSVGLA 120 ;
 Db 61 LDQOSIVHIVQRPWKQEMNATGGDPRAAGGEREPOLSTTRVDLSSVLPGSVGLA 120 ;
 Qy 121 VILHTDSRKSPSPAGSPAGSRYNSPYVYKPCQVPGKLRVQSCRAQTLTQGP 180 ;
 Db 121 VILHTDSRKSPSPAGSPAGSRYNSPYVYKPCQVPGKLRVQSCRAQTLTQGP 180 ;
 Qy 181 SCWDVLLPNRMGSQCPICGTSIAEFFKCGAHPSTDKEPVALHILANTSRNITCIT 240 ;
 Db 179 ----- ;
 Qy 241 CTDVRSPLVUQCNRSRHVICDCPHLYCWRTRNDQPHDIPOLGSLPCVAGCPNSLIKE 300 ;
 Db 213 CTDVRSPLVUQCNRSRHVICDCPHLYCWRTRNDQPHDIPOLGSLPCVAGCPNSLIKE 300 ;
 Qy 301 LHHFRILGEQNYQQGAEEVULQMGVLCPRPGAGLPEPDQDKTCCEGENGLGC 360 ;
 Db 273 LHHFRILGEQNYQQGAEEVULQMGVLCPRPGAGLPEPDQDKTCCEGENGLGC 360 ;
 Qy 361 GFAFCRECKEAYHEGCSAVFASGTTQAYRDRAAEQRWEASKETIKKTKPCR 420 ;
 Db 333 GFAFCRECKEAYHEGCSAVFASGTTQAYRDRAAEQRWEASKETIKKTKPCR 420 ;
 Qy 421 CHVPEVKNGGCMHMKCPOPOCRLEWCNWCNGCEMNVRVCGMDHFDV 465 ;
 Db 393 CHVPEVKNGGCMHMKCPOPOCRLEWCNWCNGCEMNVRVCGMDHFDV 437 ;
 ; RESULT 4
 US-09-601-844B-4 ; Sequence 3, Application US/09949016
 ; Sequence 4, Application US/09601844B

Db 301 LHHFRILGEQNYQQGAEEVULQMGVLCPRPGAGLPEPDQDKTCCEGENGLGC 360 ;
 Qy 361 GFAFCRECKEAYHEGCSAVFASGTTQAYRDRAAEQRWEASKETIKKTKPCR 420 ;
 Db 361 GFAFCRECKEAYHEGCSAVFASGTTQAYRDRAAEQRWEASKETIKKTKPCR 420 ;
 Qy 421 CHVPEVKNGGCMHMKCPOPOCRLEWCNWCNGCEMNVRVCGMDHFDV 465 ;
 Db 421 CHVPEVKNGGCMHMKCPOPOCRLEWCNWCNGCEMNVRVCGMDHFDV 465 ;
 ; RESULT 3
 US-09-601-844B-4 ; Sequence 3, Application US/09949016
 , Sequence 4, Application US/09601844B

PRIOR APPLICATION NUMBER: US/09/949,016
 PRIOR FILING DATE: 2000-04-14
 PRIOR FILING DATE: 2000-10-20
 PRIOR FILING DATE: 2000-10-03
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 6833
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6853

Query Match 92.6%; Score 2405; DB 4; Length 437;
Best Local Similarity 94.0%; Pred. No. 9.6e-232; Mismatches 0; Indels 28; Gaps 1;
Matches 437; Conservative 0; Mismatches 0; Indels 149; Gaps 1;

Qy 1 MIVFVFNSSGFPVEVDSDTSIFOLKEVAKRQGPADOLRVIFAGKELRNDDWTWONCD 60
Db 1 MIVFVFNSSHGPVEVDSDTSIFOLKEVAKRQGPADOLRVIFAGKELRNDDWTWQ--- 57

Qy 61 LDQOSIVHIVQRPWRKGQEMMAGGDPRNAGGCEREPOLITRVLSSVLPGSVGLA 120
Db 61 LDQOSIVHIVQRPWRKGQEMMAGGDPRNAGGCEREPOLITRVLSSVLPGSVGLA 120

Qy 121 VILHTDSRKDSPPAGSPAGRSIYNSPYVYCKGPQCORVQPGKLRVQCSTCROATLTQGP 180
Db 121 VILHTDSRKDSPPAGSPAGRSIYNSPYVYCKGPQCORVQPGKLRVQCSTCROATLTQ--- 178

Qy 181 SCWDDVLIPNMSGCSQSPHCPGTSABFFKCGAHTSKETPVALTHIATNSRNITCT 240
Db 179 --- BFFKCGAHTSKETPVALTHIATNSRNITCT 212

Qy 241 CTDVRSPVLUVQCNCSRHVICLDCPHUVCVTLANDRQPHDQLGSLPCVAGCPNSLIKE 300
Db 241 CTDVRSPVLUVQCNCSRHVICLDCPHUVCVTLANDRQPHDQLGSLPCVAGCPNSLIKE 300

Qy 213 CTDVRSPVLUVQCNCSRHVICLDCPHUVCVTLANDRQPHDQLGSLPCVAGCPNSLIKE 272
Db 301 LHFRTRIGEEQNYQOYGAECVLUQMGVLCPRPGAGHLPEPDQRKVTCBGGNGLGC 360

Qy 273 LHFRTRIGEEQNYQOYGAECVLUQMGVLCPRPGAGHLPEPDQRKVTCBGGNGLGC 332

Qy 361 GFAFCRECKEAYHEGCSAVEASGTTQAYRUDERAEQARWEASKETIKTTKPCP 420
Db 333 GFAFCRECKEAYHEGCSAVEASGTTQAYRUDERAEQARWEASKETIKTTKPCP 392

Qy 421 CHVPUVKNGGCHMKPQPQCRLEWCNGGCEWRVRCMDHWFDV 465
Db 393 CHVPUVKNGGCHMKPQPQCRLEWCNGGCEWRVRCMDHWFDV 437

RESULT 5
US-09-949-016-6854 Application US/09949016
; Sequence 6834, Application US/09949016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C100107
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 6054
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6854

Query Match 65.4%; Score 1696.5; DB 4; Length 316;
Best Local Similarity 68.0%; Pred. No. 4.2e-161; Mismatches 0; Indels 149; Gaps 1;
Matches 316; Conservative 0; Mismatches 0; Indels 149; Gaps 1;

Qy 1 MIVFVFNSSGFPVEVDSDTSIFOLKEVAKRQGPADOLRVIFAGKELRNDDWTWONCD 60
Db 1 MIVFVFNSSHGPVEVDSDTSIFOLKEVAKRQGPADOLRVIFAGKELRNDDWTWQ--- 57

Qy 61 LDQOSIVHIVQRPWRKGQEMMAGGDPRNAGGCEREPOLITRVLSSVLPGSVGLA 120
Db 61 LDQOSIVHIVQRPWRKGQEMMAGGDPRNAGGCEREPOLITRVLSSVLPGSVGLA 120

Qy 121 VILHTDSRKDSPPAGSPAGRSIYNSPYVYCKGPQCORVQPGKLRVQCSTCROATLTQGP 180
Db 121 VILHTDSRKDSPPAGSPAGRSIYNSPYVYCKGPQCORVQPGKLRVQCSTCROATLTQ--- 178

Qy 181 SCWDDVLIPNMSGCSQSPHCPGTSABFFKCGAHTSKETPVALTHIATNSRNITCT 240
Db 179 --- BFFKCGAHTSKETPVALTHIATNSRNITCT 212

Qy 241 CTDVRSPVLUVQCNCSRHVICLDCPHUVCVTLANDRQPHDQLGSLPCVAGCPNSLIKE 300
Db 241 CTDVRSPVLUVQCNCSRHVICLDCPHUVCVTLANDRQPHDQLGSLPCVAGCPNSLIKE 300

Qy 361 GFAFCRECKEAYHEGCSAVEASGTTQAYRUDERAEQARWEASKETIKTTKPCP 420
Db 333 GFAFCRECKEAYHEGCSAVEASGTTQAYRUDERAEQARWEASKETIKTTKPCP 392

Qy 421 CHVPUVKNGGCHMKPQPQCRLEWCNGGCEWRVRCMDHWFDV 465
Db 393 CHVPUVKNGGCHMKPQPQCRLEWCNGGCEWRVRCMDHWFDV 316

RESULT 6
US-09-270-767-32183
; Sequence 32183, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 32183
; LENGTH: 117
; TYPE: PRT
; ORGANISM: *Drosophila melanogaster*
; US-09-270-767-32183

Query Match 14.3%; Score 370.5; DB 4; Length 117;
Best Local Similarity 53.3%; Pred. No. 3.8e-29; Mismatches 40; Indels 5; Gaps 2;
Matches 64; Conservative 11; Mismatches 40; Indels 5; Gaps 2;

Qy 345 PDQRKVTCGGNGLGGFAFCRECKEAYHEGCS-SAVEASGTTQAYRUDERAEQARW 403
Db 1 PDCRKICKRN---GGYVFCRNCLGQHGECLBEGTGAATNSCEYTVDPNRAEARW 56

Qy 404 BRASKETIKKTTPCPRCHVEVERUKNGGCMIMKCPQPQCRLEWCNGGCEWRVRCMDHWF 463
Db 57 DEASNVTIKVSTKPCPKRTPTERDGGCMINVCTRAGGFBCWCVQQTETWTRDCMGIAHWF 116

RESULT 7
US-09-914-259-13
; Sequence 13, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES

FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-914-259-13

Query Match 9, 3%; Score 240; DB 4; Length 503;
Best Local Similarity 27.5%; Pred. No. 3e-15; Mismatches 11; Indels 37; Gaps 13;
Matches 72; Conservative 42; MisMatches 11; Indels 37; Gaps 13;

Qy 209 FPKCGAHTPSDKEPVHLJATMSRNITCITCDVRSPLVFOQNSRHRVILCDCHLYC 268
Db 105 FPKC-AHVINPENATEAIKOKTTSOCBECBECISQQLPPDSMAGLSCGHRICMPCHYL 163
Qy 269 VTRLNDRQFVHDPOGLYSLPCVA-GCPNLSLKEIHLHFRILRGEOQN-RYQOYGBEBCVLQ 326
Db 164 STK-----IAEGLGQTISCAANGC-DILVDDVTVANLTARVVKYQQLINTSFV-E 215
Qy 327 MGVL--CPRPGCG-AGLIPPEPDKRKTCGGNGLGGFAPICRECKEAVHNG-ECSAVE 382
Db 216 CNUQRWCISVSDCTYAVKVPYAPRRVHCK----CGHVFPCAGENWIDPVKCRWL-- 267
Qy 383 ASGTTQAYRVRDEERAEDARWEAKASKETIKITKPCPRCHVPUERKGGMHMCKPOPQCR 442
Db 268 -----KKWIKCDDSETSNWTAAN-----TKCOPRSVTEIKGGGNHHWCKNQCK 315
Qy 443 LECWQNCCEMURVCMDHWFD 464
Db 316 NEFCWVCLGSWEP-HGSSWYN 335

RESULT 8

Sequence 1011; Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL010307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 111
LENGTH: 487
TYPE: PRT
ORGANISM: Human
US-09-949-016-1011

Query Match 8, 5%; Score 222; DB 4; Length 487;
Best Local Similarity 27.8%; Pred. No. 2e-13; Mismatches 71; Conservative 27; MisMatches 97; Indels 60; Gaps 13;
Matches 71; Conservative 27; MisMatches 97; Indels 60; Gaps 13;

Qy 232 NSRNNTC--ITCTDVRSPVLF-QONSRAVTCDFHLYCVTRLNDRQFVHDPOGLYSLP 288
Db 227 NSKLFLCSITFCERKLGSECMYFLBC--RHVYACTKQYFEIQIRDGQ-----VQ 274
Qy 289 CYAGCEN-----SLIKEHLHFRILRGEOQN-RYQOYGBEBCVLQMGSTL-CPRPGCG 338
Db 275 CL-NCPPEPKPSVATPGQVRL-----VEAELFARYVRLLOSSLDIMADVYVCPRCCQ 328
Qy 339 AGLIPPEPDKRKTCGGNGLGGFAPICRECKEAVHNG-ECECAVFRASGTQAY----- 391
Db 329 LPVNGEPEG---CTMGCSCNFAFCPLCLITYHGVSPCTVABKMLNRLNEYLOADA 383
Qy 392 -----RVERAEEQARWEAKASKETIKITKPCPRCHVPUERKGGMHMCKPOPQCR 444
Db 384 NKRLIDQRYGKRVIOKALEEMESKEWLEROKSKCFCGGPIEKUDGCNKMTC-TGCMQY 441
Qy 445 WCMNGCCEMURVNG 459
Db 442 FCW-----ICMG 448

RESULT 10

Sequence 15410; Application US/09248796A
Patent No. 6741137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANE
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196-132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13

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OM protein - protein search, using sw model

Run on: February 23, 2005, 13:57:26 ; Search time 73.013 Seconds
(without alignments)

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Title: US-10-622-817-9

Perfect score: 2595

Sequence: 1 MIVFVRFNSSSHGPPVEVSD..... CWNCGCEWRVCMGDHWFDV 465

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cggn_5/_prodatal/1/pubpaal/US07_PUBCOMB.pep:*
- 2: /cggn_6/_prodatal/1/pubpaal/PCT_NEW_PUB.pep:*
- 3: /cggn_6/_prodatal/1/pubpaal/US06_PUB.pep:*
- 4: /cggn_6/_prodatal/1/pubpaal/US05_PUBCOMB.pep:*
- 5: /cggn_6/_prodatal/1/pubpaal/US07_NEW_PUB.pep:*
- 6: /cggn_6/_prodatal/1/pubpaal/PCFTUS_PUBCOMB.pep:*
- 7: /cggn_6/_prodatal/1/pubpaal/US08_PUBCOMB.pep:*
- 8: /cggn_6/_prodatal/1/pubpaal/US08_PUBCOMB.pep:*
- 9: /cggn_6/_prodatal/1/pubpaal/US09_PUBCOMB.pep:*
- 10: /cggn_6/_prodatal/1/pubpaal/US095_PUBCOMB.pep:*
- 11: /cggn_6/_prodatal/1/pubpaal/US09C_PUBCOMB.pep:*
- 12: /cggn_6/_prodatal/1/pubpaal/US09_NEW_PUB.pep:*
- 13: /cggn_6/_prodatal/1/pubpaal/US10_PUBCOMB.pep:*
- 14: /cggn_6/_prodatal/1/pubpaal/US10B_PUBCOMB.pep:*
- 15: /cggn_6/_prodatal/1/pubpaal/US10C_PUBCOMB.pep:*
- 16: /cggn_6/_prodatal/1/pubpaal/US10D_PUBCOMB.pep:*
- 17: /cggn_6/_prodatal/1/pubpaal/US10_NEW_PUB.pep:*
- 18: /cggn_6/_prodatal/1/pubpaal/US11_NEW_PUB.pep:*
- 19: /cggn_6/_prodatal/1/pubpaal/US60_NEW_PUB.pep:*
- 20: /cggn_6/_prodatal/1/pubpaal/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2595	100.0	465	16 US-10-473-226-2
2	2596	100.0	465	16 US-10-473-226-2
3	2596	100.0	465	17 US-10-839-688-9
4	2584	99.5	465	16 US-10-472-226-4
5	2405	92.6	437	16 US-10-776-604-4
6	870	33.6	9	US-09-785-48-4
7	544.5	21.0	386	14 US-10-239-249-2
8	373	14.4	64	15 US-10-313-203-10
9	323	12.4	56	15 US-10-313-203-17
10	263	10.1	46	9 US-09-864-761-36750
11	525	9.5	16	US-10-437-963-19978
12	242.6	9.3	604	15 US-10-425-114-55407
13	240.5	9.3	503	14 US-10-080-608A-13

ALIGNMENTS

RESULT 1 US-10-473-226-2 ; Sequence 2, Application US/10473226 ; Publication No. US20040198650A1	APPLICANT: Nsgene A/S TITLE OF INVENTION: Means for inhibiting proteolytical processing of Parkin FILE REFERENCE: 506-240-WO CURRENT APPLICATION NUMBER: US/10-473-226 CURRENT FILING DATE: 2003-09-29 PRIOR APPLICATION NUMBER: DK PA 2001 00525 PRIOR FILING DATE: 2001-03-29 PRIOR APPLICATION NUMBER: US 60/281,286 PRIOR FILING DATE: 2001-04-03 NUMBER OF SEQ ID NOS: 7 SOFTWARE: PatentIn version 3.1 SEQ ID NO: 2 LENGTH: 465 TYPE: PRT FEATURE: ORGANISM: Homo sapiens NAME/KEY: mat_peptide LOCATION: (1)..() OTHER INFORMATION: Native Parkin US-10-473-226-2	Query Match Similarity 100.0%; Score 2596; DB 16; Length 465; Best Local Similarity 100.0%; Pred. No. 2.2e-220; Matches 465; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 102_App Sequence 147673_A Sequence 63379_A Sequence 42_App Sequence 2_App Sequence 572_App Sequence 3019_App Sequence 44_App Sequence 1824_App Sequence 1824_App Sequence 140793 Sequence 133385 Sequence 148905 Sequence 38443_A Sequence 39657_A Sequence 1727_A Sequence 1374780A_330 Sequence 26515 Sequence 11378 Sequence 217796 Sequence 854_App Sequence 56_App Sequence 330_App Sequence 124556 Sequence 18451 Sequence 152161 Sequence 56248_A Sequence 168788 Sequence 56467_A Sequence 56455 Sequence 124556 Sequence 18451 Sequence 54725_A Sequence 21252_A Sequence 40231_A
QY 1 MIVFVRFNSSSHGPPVEVSDSISIQLKEWAKRQGPADQRLRVFAGELRNWDVNQCD 60 Db 1 MIVFVRFNSSSHGPPVEVSDSISIQLKEWAKRQGPADQRLRVFAGELRNWDVNQCD 60	6 1 LDQQSIVHIVORPWRKGQEMNATGGDDPRNAGGCEREPOLITRYDLISSVLPGRSVGLA 120 QY 6 1 LDQQSIVHIVORPWRKGQEMNATGGDDPRNAGGCEREPOLITRYDLISSVLPGRSVGLA 120		

RESULT 4
US-10-473-226-4
; Sequence 4, Application US/10473226
; Publication No. US20040198650A1
; GENERAL INFORMATION:
; APPLICANT: NBGene A/S
; TITLE OF INVENTION: Means for inhibiting proteolytical processing of Parkin
; FILE REFERENCE: 506-204-WO
; CURRENT APPLICATION NUMBER: US/10/473, 226
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: DK PA 2001 00525
; PRIOR FILING DATE: 2001-03-29
; PRIORITY APPLICATION NUMBER: US 6/0/281, 286
; PRIORITY FILING DATE: 2001-04-03
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1)..()
; OTHER INFORMATION: Parkin with a D126E mutation
; US-10-473-226-4

Query Match 99.5%; Score 2584; DB 16; Length 465;
Best Local Similarity 99.4%; Pred. No. 2.5e-219; Matches 463; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MIVFVRNNSHGPFPVEVDSITSIFOLKEVVAKRQGVPADOLRIVFAGKELRNDWTVQNC 60
Db 1 MIVFVRNNSHGPFPVEVDSITSIFOLKEVVAKRQGVPADOLRIVFAGKELRNDWTVQNC 60
Qy 61 LDQOSIVHIVOPWRKGQEMATGGDPRNAGGCEREPoSITRVDLSSVLPGDSVGLA 120
Db 61 LDQOSIVHIVOPWRKGQEMATGGDPRNAGGCEREPoSITRVDLSSVLPGDSVGLA 120
Qy 121 VILHDSRKSPASSPAGSISYNSPYVYCKGCPORVQSKLVRQVOSTCQATLTQGP 180
Db 121 VILHDSRKSPASSPAGSISYNSPYVYCKGCPORVQSKLVRQVOSTCQATLTQGP 180
Qy 181 SCWDDVLLPNRMGECOPRGTSARPPFKGAHTSDKETPVALTHIATNSRNITCT 240
Db 181 SCWDDVLLPNRMGECOPRGTSARPPFKGAHTSDKETPVALTHIATNSRNITCT 240
Qy 241 CTDVRSPLVLFQCNSRHVICLDCFHLYCVTRNLDRQFVHDQLGSLFCVAGCPNSLIKE 300
Db 241 CTDVRSPLVLFQCNSRHVICLDCFHLYCVTRNLDRQFVHDQLGSLFCVAGCPNSLIKE 300
Qy 301 LHHFRIGEONRYQQYGAECVLOMGGVLCPRPGGAGLIPEDQRKVTCEGNGLGC 360
Db 301 LHHFRIGEONRYQQYGAECVLOMGGVLCPRPGGAGLIPEDQRKVTCEGNGLGC 360
Qy 361 GFAFCRCKEAYHEGCSAVFASGTTQAYRVDERRAEQARWEASKETIKTTKPCP 420
Db 361 GFAFCRCKEAYHEGCSAVFASGTTQAYRVDERRAEQARWEASKETIKTTKPCP 420
Qy 421 CHVPEVKNGGCHMKCQPQCRLEWCWNCGCEWWNRVCMGDHWFDV 465
Db 421 CHVPEVKNGGCHMKCQPQCRLEWCWNCGCEWWNRVCMGDHWFDV 465

RESULT 5
US-10-776-604-4
; Sequence 4, Application US/10776604
; Publication No. US2005003305A1
; GENERAL INFORMATION:
; APPLICANT: Shimizu, Nobuyoshi
; APPLICANT: Mizuno, Yoshikuni
; TITLE OF INVENTION: DNAs or Genes Participating in Parkinson's Disease
; FILE REFERENCE: 0652_211001
; CURRENT APPLICATION NUMBER: US/10/776, 604

Query Match 99.5%; Score 2584; DB 16; Length 465;
Best Local Similarity 99.4%; Pred. No. 1.3e-68; Matches 155; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-10-776-604-4

CURRENT FILING DATE: 2004-02-12
PRIOR APPLICATION NUMBER: 09/601, 844
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: PCTJP99/00545
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: JP 10/27531
PRIOR FILING DATE: 1998-02-09
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 437
TYPE: PRT
ORGANISM: Homo sapiens
US-10-776-604-4

Query Match 92.6%; Score 2405; DB 16; Length 437;
Best Local Similarity 94.0%; Pred. No. 1.5e-203; Matches 437; Conservative 0; Mismatches 0; Indels 28; Gaps 1;

Qy 1 MIVFVRNNSHGPFPVEVDSITSIFOLKEVVAKRQGVPADOLRIVFAGKELRNDWTVQNC 60
Db 1 MIVFVRNNSHGPFPVEVDSITSIFOLKEVVAKRQGVPADOLRIVFAGKELRNDWTVQNC 60
Qy 61 LDQOSIVHIVOPWRKGQEMATGGDPRNAGGCEREPoSITRVDLSSVLPGDSVGLA 120
Db 61 LDQOSIVHIVOPWRKGQEMATGGDPRNAGGCEREPoSITRVDLSSVLPGDSVGLA 120
Qy 121 VILHDSRKSPASSPAGSISYNSPYVYCKGCPORVQSKLVRQVOSTCQATLTQGP 180
Db 121 VILHDSRKSPASSPAGSISYNSPYVYCKGCPORVQSKLVRQVOSTCQATLTQGP 180
Qy 181 SCWDDVLLPNRMGECOPRGTSARPPFKGAHTSDKETPVALTHIATNSRNITCT 240
Db 181 SCWDDVLLPNRMGECOPRGTSARPPFKGAHTSDKETPVALTHIATNSRNITCT 240
Qy 241 CTDVRSPLVLFQCNSRHVICLDCFHLYCVTRNLDRQFVHDQLGSLFCVAGCPNSLIKE 300
Db 241 CTDVRSPLVLFQCNSRHVICLDCFHLYCVTRNLDRQFVHDQLGSLFCVAGCPNSLIKE 300
Qy 301 LHHFRIGEONRYQQYGAECVLOMGGVLCPRPGGAGLIPEDQRKVTCEGNGLGC 360
Db 301 LHHFRIGEONRYQQYGAECVLOMGGVLCPRPGGAGLIPEDQRKVTCEGNGLGC 360
Qy 361 GFAFCRCKEAYHEGCSAVFASGTTQAYRVDERRAEQARWEASKETIKTTKPCP 420
Db 361 GFAFCRCKEAYHEGCSAVFASGTTQAYRVDERRAEQARWEASKETIKTTKPCP 420
Qy 421 CHVPEVKNGGCHMKCQPQCRLEWCWNCGCEWWNRVCMGDHWFDV 465
Db 421 CHVPEVKNGGCHMKCQPQCRLEWCWNCGCEWWNRVCMGDHWFDV 465

RESULT 6
US-03-785-548-4

Sequence 4, Application US/09785548
; Patent No. US2002015577A1
; GENERAL INFORMATION:
; APPLICANT: AVENTIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: COMPOSITIONS THAT CAN BE USED FOR REGULATING THE ACTIVITY OF PARKIN
; FILE REFERENCE: ST0005
; CURRENT APPLICATION NUMBER: US/09/785, 548
; CURRENT FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-785-548-4

Query Match 93.5%; Score 870; DB 9; Length 156;
Best Local Similarity 99.4%; Pred. No. 1.3e-68; Matches 155; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 GSPAGRSTIINSFVYCKGPGCORYOPGKLRVOCSTCROATLTQGSPCMDDVLLPNRMSG 194
Db 1 GSPAGRSTIINSFVYCKGPGCORYOPGKLRVOCSTCROATLTQGSPCMDDVLLPNRMSG 60
QY 195 ECOSPHCIGTSABFFKCGAHHTSDKETPVALHLATNSNITCTCIVRSPLVFCN 254
Db 61 ECOSPHCIGTSABFFKCGAHHTSDKETPVALHLATNSNITCTCIVRSPLVFCN 120
QY 255 SRVVICDCFHLYCVRLNDQFVRDPOLYSLPCV 290
Db 121 SRVVICDCFHLYCVRLNDQFVRDPOLYSLPCV 156

RESULT 7
US-10-239-249-2
; Sequence 2, Application US/10239249
; Publication No. US2003017750A1
; GENERAL INFORMATION:
; APPLICANT: HONER, MARCUS
; APPLICANT: BAUMESTER, RALF
; TITLE OF INVENTION: NEMATODES AS MODEL ORGANISMS FOR INVESTIGATING
; TITLE OF INVENTION: DISEASE, USES AND METHODS FOR FINDING SUBSTANCES AND
; TITLE OF INVENTION: GENES WHICH CAN BE USED IN TREATING SUCH DISEASES, AND
; TITLE OF INVENTION: IDENTIFICATION OF A NEMATODE GENE
; FILE REFERENCE: 02481.1004-00000
; CURRENT APPLICATION NUMBER: US/10/239,249
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: PCT/EP01/03214
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING NUMBER: 100 14 109.9
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-10-239-249-2

Query Match 21.0%; Score 544.5; DB 14; Length 386;
Best Local Similarity 28.9%; Pred. No. 2.1e-39;
Matches 129; Conservative 59; Mismatches 166; Indels 93; Gaps 13;

QY 22 SIFOLKEVAKRQGPADOLRVIPIAGKELRNDWVQNCDDQDQSIYHIVQRPRKGQEMN 81
Db 29 NIEDLTDKEVKLTHIPSDELEWVFCKGKLSKSTIMDLSLTFATQMLLPKPFNSHNNG 88
Qy 82 ATGGDDPRMAGGCEREPOSLTRVDLSSVLPGDSVGLAVILHTDSRKDSOPPAGSPAGRS 141
Db 89 AT-----TAKTTDS-----S 99

QY 142 IYNISFYVICKGPGQRVQPGKLRVQCSCTRCOATLTLQGSPCMDDVLLPNRMSGCQSHC 201
Db 100 ILCSPFYWCKN CDDVVERGKLRVQCSSTSVLVSEPVONWSDVLUKSKRIPAVCEBCT 158
Qy 202 PGTSAAEFFFKCCGAHPTSDKETPVALHLATNSNITCTCIVRSPLVFCN 261
Db 159 PGFLFAERFKC---LACNDPAHALTHVRGNQWMPTECCVCDGEKEKVIFDGCN-HITCQ 212
Qy 262 DFLPHCYVTRANDQFVHDPOLGYSUPC-VAGCNSLKLHFRIGEEQNYRQOOGA 320
Db 213 FCFRDVLISQERFVGVNQNPBHGFTIPCPYPGC-NRVWQDVHEHFMQTSSEYORKAT 321
Qy 321 EBCV-LQMGSYLCPREPGGAGLGLBP-DORKVTCCEGGNLGCGFARCRECKEAYHEGEC 377
Db 272 ERULIAVDDKGVTCPNVSCGOSFWPYDDGRSQCQ---DFFFSRKCG---FERNC 322
Qy 378 SAVERASGTTQQAIVRDERAABQARWEASKETIKKTTPCPRCHYVEKQGGMHMKCP 437
Db 323 VCOSEDDLRT-----TIDATIRRCPKCHVATERNGGCAHIC- 360

RESULT 8
US-10-311-203-10
; Sequence 10, Application US/10313203
; Publication No. US20040029134A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Wei
; APPLICANT: Nikolichev, Anatoly
; TITLE OF INVENTION: PS3-ASSOCIATED PARKIN-LIKE CYTOPLASMIC PROTEIN, AND RELATED COMPOUNDS
; FILE REFERENCE: 66106
; CURRENT APPLICATION NUMBER: US/10/313,203
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-313-203-10

Query Match 14.4%; Score 373; DB 15; Length 64;
Best Local Similarity 100.0%; Pred. No. 3e-25; Mismatches 0; Indels 0; Gaps 0;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 314 RYQQGAECVQVQGGLCPRGCGAGLIPPPDQRKVTCGGNGGCGFAFCRCKEAYH 373
Db 1 RYQQGAECVQVQGGLCPRGCGAGLIPPPDQRKVTCGGNGLGCFAFCRCKEAYH 60
QY 374 BGEC 377
Db 61 EGEC 64

RESULT 9
US-10-313-203-17
; Sequence 17, Application US/10313203
; Publication No. US20040029134A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Wei
; APPLICANT: Nikolaev, Anatoly
; TITLE OF INVENTION: P53-ASSOCIATED PARKIN-LIKE CYTOPLASMIC PROTEIN, AND RELATED COMPOUNDS
; FILE REFERENCE: 68105
; CURRENT APPLICATION NUMBER: US/10/313,203
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-313-203-17

Query Match 12.4%; Score 323; DB 15; Length 56;
Best Local Similarity 100.0%; Pred. No. 6.7e-21; Mismatches 0; Indels 0; Gaps 0;

QY 238 CTCCTDVRSPVLFQCNRSRHICLDCPHLYCVRLNDQFVRDPOLYSLPCVAGC 293
Db 1 CTCTDVRSPVLFQCNRSRHICLDCPHLYCVRLNDQFVRDPOLYSLPCVAGC 56

RESULT 10
US-09-664-761-36750
; Sequence 10, Application US/0984761
; Publication No. US20020048763A1
; GENERAL INFORMATION:

Qy 439 PQQRLRWCWNCGGCEWRVCGMDHWFD 464
Db 332 TSGGMIDWCFKCKTEWKECQDHWFN 357

RESULT 2

probable ARI-like RING zinc finger protein [imported] - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Accession: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
Nature, 402, 751-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1543 <STO>
C;Cross-references: UNIPROT:Q9SKC3 ; GB:AB002093 ; NID:94887759 ; PIDN:AAD32295.1 ; GSPDB.GN
A;Gene: At2g31770
A;Map position: 2

Query Match 8.5%; Score 220; DB 2; Length 543;
Best Local Similarity 25.9%; Pred. No. 5.9e-09; Matches 60; Conservative 33; Mismatches 83; Indels 56; Gaps 11;

Qy 235 NITCITCDVNSPVLVQCNRSRHIVLCLDFHLYCVRLND---ROFVHDIDPGYSLPC 289
Db 125 NIQCGLGFESTYREETARVSCHGHPYKCTWAGVITKIDPGGLRKVCPERS---C 178

Qy 290 VAGCPNSLIKSLHHFRILGERQNYR--QOYGAERCVLQMGWICPRGGAGIL--PE 344
Db 179 SRAVGKDMIEVNTETRYV--HEKVSYLLSISYVERGKKW---CPSPGCGYAVEGFGE 232

Qy 345 PDQRKUTCEGGNLGGFAFCRECKEAYHEG--BOSAVTAEASGTTQAYVDRERALQARN 403
Db 233 SSYYDVSLC-----CSYRCWNSEDAHASPVDCTV-----SKW 266

Qy 404 -----BAMSRETIRKTTRKCPCPRECHVPTVKNSGCMHMKPQOQCRLEMWCNC 449
Db 267 IFKNQDESENKNWNLANSKCPCECKRPIEKNDGCNHMTCSAP-CGHFRCWIC 317

RESULT 3

T00350 hypothetical protein KIAA0708 - human (fragment)
C;Species: Homo sapiens (man)
C;Accession: T00350 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
R;Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.
DNA Res., 5, 169-176, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. X. The complete
A;Reference number: 214142; MUID:98403880; PMID:9734811
A;Accession: T00350
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1553 <ISH>
A;Cross-references: UNIPROT:Q8IW73; EMBL:AB014608; NID:93327229; PIDN:BAA31683.1; PID:93
A;Experimental source: brain
C;Genetics:
A;Note: KIAA0708

Query Match 8.5%; Score 219.5; DB 2; Length 1753;
Best Local Similarity 21.4%; Pred. No. 2.8e-08; Matches 125; Conservative 57; Mismatches 181; Indels 221; Gaps 32;

Qy 1 MIVFVRFNSSHGFPVEV--DPSRS-----IFOLK 27
Db 1012 MWLILKFNQTEEVSVETLKLDSLSPELLOQAVPLATSGNGPLTLIEGQDPFPHGIVRLH 1071

RESULT 2

probable ARI-like RING zinc finger protein [imported] - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Accession: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
Nature, 402, 751-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1543 <STO>
C;Cross-references: UNIPROT:Q9SKC3 ; GB:AB002093 ; NID:94887759 ; PIDN:AAD32295.1 ; GSPDB.GN
A;Gene: At2g31770
A;Map position: 2

Query Match 8.5%; Score 220; DB 2; Length 543;
Best Local Similarity 25.9%; Pred. No. 5.9e-09; Matches 60; Conservative 33; Mismatches 83; Indels 56; Gaps 11;

Qy 235 NITCITCDVNSPVLVQCNRSRHIVLCLDFHLYCVRLND---ROFVHDIDPGYSLPC 289
Db 125 NIQCGLGFESTYREETARVSCHGHPYKCTWAGVITKIDPGGLRKVCPERS---C 178

Qy 290 VAGCPNSLIKSLHHFRILGERQNYR--QOYGAERCVLQMGWICPRGGAGIL--PE 344
Db 179 SRAVGKDMIEVNTETRYV--HEKVSYLLSISYVERGKKW---CPSPGCGYAVEGFGE 232

Qy 345 PDQRKUTCEGGNLGGFAFCRECKEAYHEG--BOSAVTAEASGTTQAYVDRERALQARN 403
Db 233 SSYYDVSLC-----CSYRCWNSEDAHASPVDCTV-----SKW 266

Qy 404 -----BAMSRETIRKTTRKCPCPRECHVPTVKNSGCMHMKPQOQCRLEMWCNC 449
Db 267 IFKNQDESENKNWNLANSKCPCECKRPIEKNDGCNHMTCSAP-CGHFRCWIC 317

RESULT 3

T16477 hypothetical protein F56D2.5 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Accession: T16477 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
R;Ji, Z.
submitted to the EMBL Data Library, August 1994
A;Description: The sequence of *C. elegans* cosmid F56D2.
A;Reference number: Z18519
A;Accession: T16477
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1437 <DUZ>
A;Cross-references: UNIPROT:Q20871; EMBL:U13644; NID:9532100; PIDN:91945502; PIDN:AAB5268:
A;Experimental source: strain Bristol N2; clone F56D2
C;Genetics:
A;Gene: C18P56D2.5
A;Map position: 3
A;Introns: 41/3; 134/3; 185/3; 223/3; 254/2; 287/2; 414/3

Query Match 7.9%; Score 205; DB 2; Length 437;
Best Local Similarity 20.2%; Pred. No. 6.3e-08; Matches 104; Conservative 66; Mismatches 169; Indels 176; Gaps 28;

Qy 18 DSDTSIFOLKEVVAKRCGVPAQDOLRVIFASKE-----RNDWTVWONQDLDQQSIVHIVQRPW 75
Db 3 DRDQIYEL-----BALESVRLREKLAKSDDNSDKNARI-OQIIEV-----42

Qy 76 KGQEMNATGGDPQRNAAAGCEREPQLTRVTLSSVLSRPSDGSVGLAVLHTDSRKDSPPAG 135
Db 43 -----GFDNLIDFTVTGTSDFGDQDFHFLDLP-----PIRLKFHLNDYPTV 88

Qy 136 SPGRSIVNSFVYVKGCPGCPVRQPCSKLVRQCATITLTOGPSCMDVUJPNRMSGE 195

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OM protein - protein search, using sw model
Run on: February 23, 2005, 13:33:04 ; Search time 88.371 Seconds
(without alignments)

Title: US-10-622-817-9
Perfect score: 2596
Sequence: I MIVFVRFNSSHGPVEVDSL.....CWNCGCEWWNRVCMDHWFDV 465

scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:
1: uniprot_sprot:
2: uniprot_trembl:
2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2596	100.0	465	1 PRKN_HUMAN
2	2218	85.4	465	1 PRKN_RAT
3	2105	83.0	464	1 PRKN_MOUSE
4	1115	43.0	203	2 Q8N12
5	1060	40.8	194	2 Q55M07
6	1058.5	40.8	482	2 Q55T4
7	1058.5	40.8	482	2 Q7RTX7
8	1049	40.4	514	2 Q7Q591
9	1024	39.4	177	2 Q8N141
10	957	36.9	177	2 Q8K5C2
11	544.5	21.0	386	2 Q8KU3
12	544.5	20.9	162	2 Q86LE7
13	485	18.7	111	2 Q8VHY5
14	420.5	16.2	120	2 Q7TPF8
15	382	14.7	78	2 Q8KLN5
16	284	10.9	50	2 Q5G216
17	256	9.9	520	2 Q5T4B6
18	250.5	9.6	562	2 Q84RRO
19	249.5	9.6	492	2 Q68F65
20	246	9.5	525	2 Q653SB
21	240.5	9.3	503	1 ARI1_DROME
22	240	9.2	492	2 Q7T355
23	240	9.2	511	2 Q9VT94
24	238.5	9.2	527	2 Q7QGU7
25	236.5	9.1	445	2 Q8CRJ4
26	236.5	9.1	533	2 Q6W8M5
27	236.5	9.1	503	1 ARI1_MOUSE
28	236.5	9.1	557	1 ARI1_HUMAN
29	234.5	9.0	527	2 Q6PFJ9
30	232.5	9.0	492	1 ARI2_MOUSE
31	8.9	491	2 Q6GLD3	Q9gl03_xenopus_tro

RESULT 1	
PRKN_HUMAN	STANDARD; PRT; 465 AA.
ID	Q8N143; Q8BN44; Q8WW07;
AC	060260;
DT	25-OCT-2004 (Rel. 45, Created)
DT	25-OCT-2004 (Rel. 45, Last sequence update)
DT	25-OCT-2004 (Rel. 45, Last annotation update)
DR	Parkin (EC 6.3.2.-) (Ubiquitin E3 ligase PRKN) (Parkinson disease protein 2) (Parkin protein 2) (Parkinson disease protein 2).
GN	Name=PRK2; Synonyms=PRKN;
OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9605;
RN	[1] TISSUE=Fetal brain, and skeletal muscle; MEDLINE=9560156; DOI=10.1038/33416;
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND INVOLVEMENT IN JUVENILE PARKINSON'S DISEASE.
RC	Mitohoma S., Yokochi M., Mizuno Y., Shimizu N.; Minohara T., Asakawa S., Hattori N., Matsubine H., Yamamura Y..
RK	"Mutations in the parkin gene cause autosomal recessive juvenile parkinsonism.";
RA	Nature 392:605-608(1998).
RL	[2]
RN	SEQUENCE FROM N.A. (ISOFORM 5).
RC	TISSUE=Testis;
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strasserberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klauniger R.D., Collins F.S., Wagner L., Sheehan C.M., Schuler G.D., Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordon H., Moore T., Max S.I., Wang J.J., Heiher F., Diatchenko L., Marusina K., Farmer A.N., Rubin G.M., Hong L., Stapleton M., Soates M.B., Benaldo M., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Yoshiaki S., Carninci P., Prange C., Raha S.S., Loquelandano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.N., Gay L.J., Hollyk S.W., Villalon D.K., Muzny D.M., Sodergren E.B.J., Lu X., Gibbs R.A., Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green D.P., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialius D.E., Schnarch A., Schein J.E., Jones J.S.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human RT proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)."
RN	[4]

- RP FUNCTION IN UBIQUITINATION.
RX PubMed=10973942; DOI=10.1074/jbc.C000447200;
RA Imai Y., Soda M., Takahashi R.;
RT "Parkin suppresses unfolded protein stress-induced cell death through its E3 ubiquitin-protein ligase activity.";
RL J. Biol. Chem. 275:35661-35664(2000).
RN [15]
- RP FUNCTION AND CHARACTERIZATION OF VARIANTS PD PRO-42 AND ARG-240.
RX PubMed=10888818; DOI=10.1038/77060;
RA Shimura H., Hattori N., Kubo S.-I., Mizuno Y., Asakawa S.,
RA Minoshima S., Shinizu N., Iwai K., Chiba T., Tanaka K., Suzuki T.;
RT "Familial Parkinson disease gene product, parkin, is a ubiquitin-protein ligase.";
RL Nat. Genet. 25:302-305(2000).
RN [16]
- RP FUNCTION, AND INVOLVEMENT IN CANCER.
RX PubMed=1271539; DOI=10.1073/pnas.0931252100;
RA Cesari R., Martin E.S., Calin G.A., Penitmaili F., Bichi R.,
RA McAdams H., Trapasso F., Drusco A., Shimizu M., Mascullo V.,
D'Andriulli G., Scambia G., Picchio M.C., Alder H., Godwin A.K.,
RA Croce C.M.;
RT "parkin, a gene implicated in autosomal recessive juvenile parkinsonism, is a candidate tumor suppressor gene on chromosome 6q25-
q27.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5956-5961(2003).
RN [17]
- RP FUNCTION, INTERACTIONS WITH FBXW7 AND CULL, AND UBIQUITINATION OF CYCLIN E.
RX PubMed=12428165;
RA Staropoli J.F., McDermott C., Martinat C., Schulman B., Demireva E.,
RA Abelliovich A.;
RT "Parkin is a component of an SCF-like ubiquitin ligase complex and protects postmitotic neurons from kainate excitotoxicity.";
RN [18]
- FUNCTION: UBIQUITINATION, AND S-NITROSYLATION.
RX Dawson V.L., Thomas B., Li X., Pletnikova O., Troncoso J.C., Marsh L.,
RT "S-nitrosylation of parkin regulates ubiquitination and compromises parkin's protective function.";
RN Science 304:1328-1331(2004).
RN [19]
- RP SUBCELLULAR LOCATION.
RX PubMed=10319893;
- RA Shimura H., Hattori N., Kubo S.-I., Yoshiikawa M., Kitada T.,
RA Matsumine H., Asakawa S., Minoshima S., Yamamura Y., Shimizu N.,
RT Mizuno Y.;
RT "Immunohistochemical and subcellular localization of Parkin Protein: absence of Protein in autosomal recessive juvenile parkinsonism patients.";
RL Ann. Neurol. 45:668-672(1999).
RN [10]
- RP INTERACTIONS WITH UBE2L6 AND SEPT5, AND UBIQUITINATION OF SEPT5.
RX PubMed=1108524; DOI=10.1073/pnas.24037797;
RT "Parkin functions as an E2-dependent ubiquitin-protein ligase and promotes the degradation of the synaptic vesicle-associated protein, CDCrel-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:13354-13359(2000).
RN [11]
- RP UBIQUITINATION OF GPR37.
RX MEDLINE=21332586; PubMed=11439185; DOI=10.1016/S0092-8674(01)00407-X;
RA Imai Y., Suda M., Inoue H., Hattori N., Mizuno Y., Takahashi R.;
RT "An unfolded putative transmembrane polypeptide, which can lead to endoplasmic reticulum stress, is a substrate of Parkin.";
RL Cell 105:891-902(2001).
RN [12]
- RP INTERACTION: UBIQUITINATION OF SNCAP, CHARACTERIZATION OF VARIANTS AR-JP ARG-240; CYS-256, TRP-275 AND ASN-415, AND MUTAGENESIS OF CYS-337; CYS-421 AND CYS-431.
RX Published=11590339; DOI=10.1089/mn.2001.1144;
RA Chung K.K., Zhang Y., Lim K.L., Tanaka Y., Huang H., Gao J.,
RA
- RA Ross C.A., Dawson V.L., Dawson T.M.,
RT "Parkin ubiquitinates the alpha-synuclein-interacting protein, synphilin-1: implications for Lewy-body formation in Parkinson disease.";
RL Nat. Med. 7:1144-1150(2001).
RN [13]
- RP INTERACTIONS WITH STUBL AND HSP70, AND UBIQUITINATION OF STUBL.
RX PubMed=12150907;
RA Shimura H., Hatakeyama S., Akagi T., Hashikawa T., Nakayama K.-I., Takahashi R.;
RT "CHIP is associated with Parkin, a gene responsible for familial Parkinson's disease, and enhances its ubiquitin ligase activity.";
RL Mol. Cell 10:55-67(2002).
RN [14]
- RP INTERACTION WITH SYT1, CHARACTERIZATION OF VARIANT PD GLY-289, AND MUTAGENESIS OF CYS-418.
RX PubMed=1225565; DOI=10.1093/hmg/ddg269;
RA Kuylen D.P., Scopes D.R., Nguyen D., Pulst S.M.;
RT "The autosomal recessive juvenile Parkinson disease gene product, parkin, interacts with and ubiquitinates synaptotagmin XI.";
RL Hum. Mol. Genet. 12:2587-2597(2003).
RN [15]
- RP UBIQUITINATION OF AN O-LINKED GLYCOSYLATED ISOFORM OF SNCAP, SUBCELLULAR LOCATION, AND CHARACTERIZATION OF VARIANTS PD PRO-42 AND ARG-240.
RX PubMed=11431533; DOI=10.1126/science.1060627;
RA Shimura H., Schlossmacher M.G., Hattori N., Frosch M.P., Trockenbacher A., Schneider R., Mizuno Y., Kosik K.S., Selkoe D.J.;
RT "Ubiquitination of a new form of alpha-synuclein by parkin from human brain: implications for Parkinson's disease.";
RL Science 293:263-269(2001).
RN [16]
- RP INVOLVEMENT IN CANCER.
RX PubMed=14614460; DOI=10.1038/sj.onc.1207072;
RA Denison S.R., Wang F., Becker N.A., Schuele B., Koch N.,
RT Phillips L.A., Klein C., Smith D.I.;
RT "Alterations in the common fragile site gene Parkin in ovarian and other cancers.";
RL Oncogene 22:8370-8378(2003).
RN [17]
- RP REVIEW
RX PubMed=15229644; DOI=10.1038/sj.emboj.7400188;
RA Kahle P.J., Haass C.;
RT "How does Parkin ligate ubiquitin to Parkinson's disease?";
RL EMBO Rep. 5:681-685(2004).
RN [18]
- RP STRUCTURE BY NMR OF 1-76, AND INTERACTION WITH PSD4.
RX PubMed=12334850; DOI=10.1038/sj.emboj.764;
RA Sakata E., Yamaguchi Y., Kurimoto E., Kikuchi J., Yokoyama S.,
RA Yamada S., Kawahara H., Yokosawa H., Hattori N., Mizuno Y., Tanaka K.,
RT Kato K.;
RT "Parkin binds the Rpn10 subunit of 26S proteasomes through its ubiquitin-like domain.";
RL EMBO Rep. 4:301-306(2003).
RN [19]
- RP REVIEW ON VARIANTS.
RX PubMed=44976155; DOI=10.1093/hmg/ddh089;
RA Mata J.F., Lockhart P.J., Farmer M.J.;
RT "Parkin genetics: one model for Parkinson's disease.";
RL Hum. Mol. Genet. 13:R127-R133(2004).
RN [20]
- RP VARIANT AR-JP ARG-240.
RX PubMed=9731209;
RA Hattori N., Matsumine H., Asakawa S., Kitada T., Yoshino H.,
RA Elibol B., Brookes A.J., Yamamura Y., Kobayashi T., Wang M.,
RA Yoritaka A., Minoshima S., Shimizu N., Mizuno Y.;
RT "Point mutations (Trp240Arg and Glu318Stop) in the Parkin gene.";
RL Biochem. Biophys. Res. Commun. 249:754-758(1998).
RN [21]
- RP ERRATUM.
RA Hattori N., Matsumine H., Asakawa S., Kitada T., Yoshino H.,
RA Elibol B., Brookes A.J., Yamamura Y., Kobayashi T., Wang M.,
RA Yoritaka A., Minoshima S., Shimizu N., Mizuno Y.;

RL	Biochem. Biophys. Res. Commun.	251:666-666(1998).
RN	Query Match [22]	100.0%; Score 2596; DB 1; Length 455;
	Best Local Similarity 100.0%; Pred. No. 1.3e-195;	Matches 465; Conservative 0; Mismatches 0; Index 0; Gap
OY	1 MIVFVRENSSHGPVEVSDTSFOLKEVKWAKRQGPVADQLRVFASCEKBLRDWTWON	
DB	1 MIVFVRENSSHGPVEVSDTSFOLKEVKWAKRQGPVADQLRVFASCEKBLRDWTWON	
OY	61 LDQOSITVIIVQRMWKKGEMNAATGDDPFRNAAAGCGERPOSUTRDVLSSVLRGSIV	
DB	61 LDQOSITVIIVQRMWKKGEMNAATGDDPFRNAAAGCGERPOSUTRDVLSSVLRGSIV	
OY	121 VLAHTDSRKDSSPPAGSPAGRSIYNSFYVCKGKGCQRVOPGKURVQSCSTCRQALTLTC	
QY	121 VLAHTDSRKDSSPPAGSPAGRSIYNSFYVCKGKGCQRVOPGKURVQSCSTCRQALTLTC	
DB	121 VLAHTDSRKDSSPPAGSPAGRSIYNSFYVCKGKGCQRVOPGKURVQSCSTCRQALTLTC	
OY	181 SCWDDVLLPNRMSGECPSPHCPTSAEFPKCGAHPTSKETPVALHLJATSNRNTCC	
DB	181 SCWDDVLLPNRMSGECPSPHCPTSAEFPKCGAHPTSKETPVALHLJATSNRNTCC	
OY	241 CTDVRSPLVLFQCNRSRATCLDPFLYCVTRNDRQFHDPOLQYSIPLVACCPNSLII	
DB	241 CTDVRSPLVLFQCNRSRATCLDPFLYCVTRNDRQFHDPOLQYSIPLVACCPNSLII	
OY	301 LHHIFRILGEEQYRYQQYGAEECVLQMGGVLCRPGCGAGLIPEDPDKRIVTCEGGNGI	
DB	301 LHHIFRILGEEQYRYQQYGAEECVLQMGGVLCRPGCGAGLIPEDPDKRIVTCEGGNGI	
OY	361 GFAFCRECKEAVYIEGCCAVFELSGTTQAYRDERALEQARWEAKETIKTTKCC	
DB	361 GFAFCRECKEAVYIEGCCAVFELSGTTQAYRDERALEQARWEAKETIKTTKCC	
OY	421 CHVPVKQGCMIMKCPQPQCRLEWCMGCHENRVCNGDHMFDV 465	
DB	421 CHVPVKQGCMIMKCPQPQCRLEWCMGCHENRVCNGDHMFDV 465	
RESULT 2		
PRKN RAT	PRKN RAT STANDARD; PRT; 465 AA.	
ID	PRKN RAT	
AC	Q9JK66; Q8K5C3; Q8K5C5; Q8K5G6; Q8VHY6; Q9JU11; Q9JM64;	
DT	25-OCT-2004 (Rel. 45, Created)	
DT	25-OCT-2004 (Rel. 45, Last sequence update)	
DT	25-OCT-2004 (Rel. 45, Last annotation update)	
DE	Parkin (EC 6.3.2.1) (Ubiquitin E3 ligase PRKN).	
GN	Name=Park2; Synonyms=ark2;	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus	
OX	NCBI_TaxId=10116;	
RN	[1] SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6).	
RP	STRAIN=Sprague-Dawley;	
RC	SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6).	
RX	MIDDLEWARE=20199898; PubMed=10737637;	
RA	Gu W.-J., Abbas N., Leguine M.Z., Parent A., Pradier L., Bohme G.A., Agid Y., Hirach E.C., Rainman-Vozari R., Brice A.; Cloning of rat parkin cDNA and distribution of parkin in rat brain.	
RT	J. Neurochem. 74:1773-1776 (2000).	
RL	Hettori N., Wang M., Mizuno Y.; The expression of parkin mRNA in developing, adult and ageing rat.	
RN	SEQUENCE FROM N.A. (ISOFORM 1).	
RC	SEQUENCE FROM N.A. (ISOFORM 1).	
RP	"The expression of parkin mRNA in developing, adult and ageing rat."	

CNS.?
 RL submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1)
 RC STRAN=Sprague-Dawley; TISSUE=Brain;
 RA Suda M.; Imai Y.; Takahashi R.;
 RT "Molecular cloning of rat Parkin gene.";
 RL Submitted (APR-2000) to the EMBL/Genbank/DBJ database.
 CC - FUNCTION: Functions within a multi-protein E3 ubiquitin ligase
 complex, catalyzing the covalent attachment of ubiquitin moieties
 onto substrate proteins. These substrates include SYT1, CCNE1, and
 GPR37. STUB1, a 22 kDa O-linked glycosylated isoform of SNCAIP and
 SPT15. May play a more general role in the ubiquitin proteasomal
 pathway by participating in the removal and/or detoxification of
 abnormally folded or damaged protein. Loss of this ubiquitin
 ligase activity appears to be the mechanism underlying
 pathogenesis of AR-JP. May protect neurons against alpha synuclein
 toxicity, proteasomal dysfunction, GPR37 accumulation, and
 kainate-induced excitotoxicity. May play a role in controlling
 neurotransmitter trafficking at the presynaptic terminal and in
 calcium-dependent exocytosis. Regulates cyclin E during neuronal
 apoptosis. May represent a tumor suppressor gene (By Similarity).
 CC - SUBUNIT: Forms an E3 ubiquitin ligase complex, consisting of PARK2, CUL1 and
 UBE2L6. Part of a SCF-like complex, consisting of PARK2, CUL1 and
 RBXW7. Interacts with SNCAIP. Binds to the C2A and C2B domains of
 SYT1. Interacts and regulates the turnover of SPT15. Part of a
 complex, including STUB1, HSP70, and GPR37. The amount of STUB1 in
 the complex increases during ER stress. STUB1 promotes the
 dissociation of HSP70 from PARK2 and GPR37, thus facilitating
 PARK2-mediated GPR37 ubiquitination. HSP70 transiently associates
 with unfolded GPR37 and inhibits the E3 activity of PARK2, whereas,
 STUB1 enhances the E3 activity of PARK2 through promotion
 of dissociation of HSP70 from PARK2-GPR37 complexes. Interacts
 with PSM4 (By Similarity).
 CC - SUBCELLULAR LOCATION: Cytoplasmic. Expressed in the endoplasmic
 reticulum, dendrites, some presynaptic terminals and in
 postsynaptic densities (By similarity).
 CC - ALTERNATIVE PRODUCTS:
 CC - Event=Alternative splicing; Named isoform=**b=6**;
 CC - Name=**1**;
 CC - IsoId=Q9JK66-1; Sequence=Displayed;
 CC - Name=**2**;
 CC - IsoId=Q9JK66-2; Sequence=vSP_011722, VSP_011723;
 CC - Name=**3**;
 CC - IsoId=Q9JK66-3; Sequence=vSP_011717;
 CC - Name=**4**;
 CC - IsoId=Q9JK66-4; Sequence=vSP_011718;
 CC - Name=**5**;
 CC - IsoId=Q9JK66-5; Sequence=vSP_011719;
 CC - Name=**6**;
 CC - IsoId=Q9JK66-6; Sequence=vSP_011717, VSP_011720, VSP_011721;
 CC - TISSUE SPECIFICITY: Largely confined to neuronal elements,
 including fibers and neuropil. Highly expressed at the forebrain
 level, in pyramidal cells of layer V, in various cortical regions
 and cerebellum. Expressed in the nucleus of diagonal band of
 Broca, nucleus basalis, bed nucleus of the stria terminalis, and
 olfactory tubercle. Moderate expression is seen in most neurons of
 the subthalamic nucleus, heart, skeletal muscle and testis.
 Moderate expression was found in frontal cortex, parietal cortex,
 cerebellum, heart, skeletal muscle and testis.
 CC - DOMAIN: The ubiquitin-like domain binds the PSM4 subunit of 26S
 proteasomes (By similarity).
 CC - PTM: Auto-ubiquitination in an E2-dependent manner leading to its
 own degradation (By similarity).
 CC - PTM: S-nitrosylation (By similarity).
 CC - SIMILARITY: Contains 2 IBR-type zinc fingers.
 CC - SIMILARITY: Contains 1 ubiquitin-like domain.
 CC - CAUTION: Has been said to contain 2 RING fingers, but these are
 not found by any domain detection methods.
 CC -
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 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 RT

ב' ט

181 SCWDQVLILPRMMSGECQSPHCPGTSAAFFPKCGAHPTSDKETPVALTHIATNSRNITCIT
 181 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 181 SCWDDVLILPRNRMMSGECQSPDPCGTRABFEFKGAHPTSDKOTSVALNLTNSRNIPCA 240
 241 CTDVRSPLVFOCNSRHIVCLDCPHLYCVTRULANDRPTVHDOLQYSLPCVAGCPNSLIKE 300
 241 |||||:|||||:|||||:|||||:|||||:|||||:|||||:
 241 CTDVNPVLVFOCNSRHIVCLDCPHLYCVTRULANDRPTVHDOLQYSLPCVAGCPNSLIKE 300
 301 LHHRLIGEQQTYQQGAEBCVLOLNGVVAEPRPGCAGHLPERDOKYTCESGNGLGC 360
 301 LHHFRILQREQMYQQGAEBCVLOLNGVVAEPRPGCAGHLPERDOKYTCESGNGLGC 360
 361 GFAFCRECKEYHEGECSAVFASGTTQAYRUDERASAEQRWEASKEVKITKTTPCR 420
 361 |||||:|||||:|||||:|||||:|||||:
 361 GFVFCDKKEAHEGCDMSMEASGATSQAYRVDRQAESQRWEASKETVKITKTTPCR 420
 421 CHPVEKNGGCMHKCTQOPORLEWCWNCCGEMWVCMGDHWFDV 465
 421 |||||:|||||:
 421 CNVPIERKNGGCMHKCPQPOCKEWCVNCGEWNRACMGDHWFDV 465

RT familial Parkinson's disease."

J. BIOMOL. NMR. 25:153-156 (2003).

- I- FUNCTION: Catalyzes the covalent attachment of ubiquitin moieties onto substrate proteins. These substrates include SYT1, CCM1, GPR37, STUBL, a 22 kDa O-linked glycosylated isoform of SNCAIP and SEPT5. May play a more general role in the ubiquitin proteasomal pathway by participating in the removal and/or detoxification of abnormally folded or damaged protein. Loss of this ubiquitin ligase activity appears to be the mechanism underlying pathogenesis of AR-IP. May protect neurons against alpha synuclein toxicity, proteasomal dysfunction, GPR37 accumulation, and kainate-induced excitotoxicity. May play a role in controlling neurotransmitter trafficking at the presynaptic terminal and in calcium-dependent exocytosis. Regulates cyclin E during neuronal apoptosis. May represent a tumor suppressor gene (By similarity).

- I- PATHWAY: Ubiquitin conjugation; third step.

- I- SUBUNIT: Forms an E3 ubiquitin ligase complex with UBE2L3 or UBE2L6. Part of a SCF-like complex, consisting of PARK2, CUL1 and FBXW7. Interacts with SNCAIP. Binds to the C2A and C2B domains of SYT1. Interacts and regulates the turnover of SEPT5. Part of a complex, including STUBL, HSP70, and GPR37. The amount of STUBL in the complex increases during ER stress. STUBL promotes the dissociation of HSP70 from PARK2 and GPR37, thus facilitating PARK2-mediated GPR37 ubiquitination. HSP70 transiently associates with unfolded GPR37 and inhibits the E3 activity of PARK2, whereas, STUBL enhances the E3 activity of PARK2 through promotion of dissociation of HSP70 from PARK2-GPR37 complexes. Interacts with PSMd4 (By similarity).

- I- SUBCELLULAR LOCATION: Cytoplasmic. Expressed in the endoplasmic reticulum, dendrites, some presynaptic terminals and in postsynaptic densities.

- I- ALTERNATIVE PRODUCTS:

Name=1; IsoId=Q9WVS6-1; Sequence=Displayed;

Name=2; IsoId=Q9WVS6-2; Sequence=VSP_011714, VSP_011715;

Name=3; IsoId=Q9WVS6-3; Sequence=VSP_011713, VSP_011716;

- I- TISSUE SPECIFICITY: Expressed in all subdivisions of the brain. Highly expressed in brainstem, cranial nerve, pontine, cerebellar nuclei, indium griseum nuclei, reticularis, strata oriens and lacunosorum moleculare of the hippocampal CA2 region. Low levels were found in the telencephalon and diencephalon. Expressed in heart, liver, skeletal muscle, kidney and testis.

- I- DEVELOPMENTAL STAGE: In late 10 dpc weakly expressed in postmitotic neurons in the mantle layer of the developing nervous system. Expression increased at 11-12 dpc. At 15-16 dpc, as more specialized neurons and nonneuronal cells are formed, expression is more tissue specific. Expression was highest in the neurites, moderate levels were observed in the migrating postmitotic neurons in the intermediate and neopallial layers. In the diencephalon and other CNS regions, while the weakest level of expression was observed in the cell bodies. In nonneuronal tissues, high levels of expression were found in the muscle walls of the intestine, the blood vessels and the dermis.

- I- DOMAIN: The ubiquitin-like domain binds the PSMd4 subunit of 26S proteasomes (By similarity).

- I- PTM: Auto-ubiquitination in an E2-dependent manner leading to its own degradation (By similarity).

- I- PTM: S-nitrosylation.

- I- SIMILARITY: Contains 2 IBR-type zinc fingers.

- I- CAUTION: Has been said to contain 2 RING fingers, but these are not found by any domain detection methods.

CC or send an email to license@ib-sib.ch).

CC CC

CC DR

CC EMBL; AB019558; BAAB2404; 1; -

CC DR

CC EMBL; AF250293; AAC13890; 1; -

CC DR

CC EMBL; AF250294; AAC13891; 1; -

CC DR

CC PDB; 1MGB; NMR; A1-76;

CC DR

CC MGI; J355296; Park2.

CC DR

CC InterPro; IPR000626; Ubiquitin.

CC DR

CC InterPro; IPR002867; Znf_C6HC.

CC DR

CC Pfam; PF01485; IBR; 1.

CC DR

CC PROSITE; PS50053; UBIQUITIN2; 1;

CC DR

CC 3D-structure; Alternative splicing; Ligase; Metal-binding; Repeat;

CC DR

CC S-nitrosylation; Ubl conjugation; Ubl conjugation pathway; Zinc;

CC DR

CC Zinc-finger.

CC FT DOMAIN 1 76 UbiQuitin-like.

CC FT DOMAIN 204 238 STYL binding 1.

CC FT 257 293 STYL1 binding 2.

CC FT 313 377 IBR-type 1.

CC FT 400 456 IBR-type 2.

CC FT 244 261 RSPV1FOCNHRHVICLD -> SHPLLSGASVWTRPHL

CC FT (in Isoform 3). /FTId=VSP_011713.

CC FT SPV1FOCNH -> FMRMSKRTS (in Isoform 2). /FTId=VSP_011714.

CC FT VARSPUC 255 464 Missing (in Isoform 2). /FTId=VSP_011715.

CC FT VARSPUC 262 464 Missing (in Isoform 3). /FTId=VSP_011716.

CC FT CONFLICT 137 137 P -> PA (In Ref. 1 and 2; AAC13890).

CC SQ SEQUENCE 464 AA; 51617 MW; 5574A285A91B080 CRC64;

CC Query Match 83.6%; Score 2170.5; DB 1; Length 464;

CC Best Local Similarity 83.4%; Pred. No. 3.6e-162; Indels 1; Gaps 1;

CC Matches 388; Conservative 29; Mismatches 47; Indexes 1;

CC QY 1 MIVFVRPNSSHGPPVVEDSDTSIFQIKEVAKRQGPADQLRVLVAGKELRNDMTVQNC 60

CC Db 1 MIVFVRPNSSHGPPVVEDSDTSIFQIKEVAKRQGPADQLRVLVAGKELRNDMTVQNC 60

CC QY 61 LDQOSITVHTVQRPWKQGMNATGGDDPRVNAAGGEREPOLSLTRVLLSSVLPGSVGLA 120

CC Db 61 LEQOSITVHTVQRPWKQGMNATGGDDPRVNAAGGEREPOLSLTRVLLSSVLPGSVGLA 120

CC QY 121 VILHDPSRKQSPAGSPAGSPAGSIYNSFYVCKGPQCPQRVQSTCROATLTQGP 180

CC Db 121 VILHDPSRKQSPAGSPAGSPAGSIYNSFYVCKGPQCPQRVQSTCROATLTQGP 179

CC QY 181 SCWDDVLIPNRMGCGQSPPCPGTSAEFFKCGAHTSDKETPVALHLIATNSRNITC 240

CC Db 180 SCWDDVLIPNRMGCGQSPPCPGTSAEFFKCGAHTSDKETPVALHLIATNSRNITC 239

CC QY 241 CTDVRSPLVFLQCSRNRHVILCFHLYCVTRLNDQPVHPOLQSYSLPCVAGCPNLSIKE 300

CC Db 240 CTDVRSPLVFLQCSRNRHVILCFHLYCVTRLNDQPVHPOLQSYSLPCVAGCPNLSIKE 299

CC QY 301 LHHFRIGESEQNYRQCYGAEECVLQMGGMICPRPGGAGLPEPDQKTYCEGENGLC 360

CC Db 300 LHHFRIGESEQNYRQCYGAEECVLQMGGMICPRPGGAGLPEPDQKTYCEGENGLC 359

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Db	420 CNVPIEKNGGCMHMKCPQPOCKLWCWNCCENRACMDHWFDV	464	RN [2] RP SEQUENCE FROM N.A. RC TISSUE=Brain; RX MEDLINE=21869006; PubMed=11879804; DOI=10.1016/S0006-8993(02)02241-2; RA Hase A., Yamada H., Arai K., Sunada Y., Shimizu T., Matsumura K.; RT "Characterization of parkin in bovine peripheral nerve."; RL Brain Res. 930:143-149 (2002). DR EMBL: AB050701; BA870670_1; -. DR GO; GO:004842; P:ubiquitin-protein ligase activity; IEA. DR GO; GO:006512; P:ubiquitin cycle; IEA. DR InterPro; IPR003977; parkin. DR Prints; PRO1475; PARKIN. DR FT Prints; PRO1475; PARKIN. FT NON_TER 194 AA; 194 1 FT NON_TER 194 AA; 2125 MW; 9214F09FA74FAB1 CRC64;
RA	D'Agata V., Scapagnini G., Cavallaro S.;	PRT; 203 AA.	Query Match Score 100%; DB 2; Length 194; Best Local Similarity 99.5%; Pred. No. 2, 4e-75; Indels 0; Gaps 0; Matches 193; Conservative 99%; 0; Mismatches 1; Indels 0; Gaps 0;
RL	Submitted (May-2001) to the EMBL/GenBank/DBJ databases.		
DR	AF381284; AMM21459_1; -.		
DR	GO:0009432; P:ubiquitin-protein ligase activity; IEA.		
DR	GO:000512; P:ubiquitin cycle; IEA.		
DR	InterPro; IPR003977; parkin.		
DR	Prints; PRO1475; PARKIN.		
DR	PF01085; IBR; 1.		
DR	SMART; SM00647; IBR; 1.		
SQ	SEQUENCE FROM N.A.		
Query	192 MSGECOSPHPCGTSAAEPPFKCQAHPSDKETPVALTHIATNSRNITCITCDVSPVLFV 251	PRT; 203 AA.	Query Match Score 1115; DB 2; Length 203; Best Local Similarity 100.0%; Pred. No. 1, 2e-79; Indels 0; Gaps 0; Matches 198; Conservative 100.0%; 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 MSGECOSPHPCGTSAAEPPFKCQAHPSDKETPVALTHIATNSRNITCITCDVSPVLFV 60		
Query	252 QNSRHVICLDFCFHLVCVTRANDRQVHDPOGLYSLPCVGPNLSIKEHHFRIGEQ 311	PRT; 194 AA.	Query Match Score 100%; DB 2; Length 194; Best Local Similarity 99.5%; Pred. No. 2, 4e-75; Indels 0; Gaps 0; Matches 193; Conservative 99%; 0; Mismatches 1; Indels 0; Gaps 0;
Db	61 QNSRHVICLDFCFHLVCVTRANDRQVHDPOGLYSLPCVGPNLSIKEHHFRIGEQ 120		
Query	312 YNRYYQQYGAEEBCVLOQGGVLCPRPGAGLIPERPPDORKVYCEGNGLGCFACRECKEA 371	PRT; 194 AA.	Query Match Score 100%; DB 2; Length 194; Best Local Similarity 99.5%; Pred. No. 2, 4e-75; Indels 0; Gaps 0; Matches 193; Conservative 99%; 0; Mismatches 1; Indels 0; Gaps 0;
Db	121 YNRYYQQYGAEEBCVLOQGGVLCPRPGAGLIPERPPDORKVYCEGNGLGCFACRECKEA 180		
Query	372 YHEGECSAVFAESGRGTTQ 389	PRT; 194 AA.	Query Match Score 100%; DB 2; Length 194; Best Local Similarity 99.5%; Pred. No. 2, 4e-75; Indels 0; Gaps 0; Matches 193; Conservative 99%; 0; Mismatches 1; Indels 0; Gaps 0;
Db	181 YHEGECSAVFAESGRGTTQ 198		
RESULT 5			
Q95M07	PRELIMINARY; PRT; 194 AA.		
AC	Q95M07; (Trembler. 19, Created)		
DT	01-DEC-2001 (Trembler. 19, Last sequence update)		
DT	01-JUN-2003 (Trembler. 24, Last annotation update)		
DE	Parkin (Fragment)		
GN	Name=parkin; Synonyms=CG10523;		
OS	Bos taurus (Bovine).		
OC	Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	SEQUENCE FROM N.A.		
RP	SEQUENCE FROM N.A.		
RA	Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Fries E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nuovo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Robin G.M., Celikiner S.; Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AY058754; AAU13983_1; -.		
DR	HSSP; Q86204; IAKR.		
DR	FlyBase; FBgn0041100; park.		
DR	GO; GO:0007005; P:mitochondrion organization and biogenesis; IMP.		
RA	Kirada T., Asakawa S., Hattori N., Matsumura H., Yamamura Y., Minoshima S., Yokochi M., Mizuno Y., Shimizu N.;		
RT	"Mutations in the parkin gene cause autosomal recessive juvenile Parkinsonism".		
RP	SEQUENCE FROM N.A.		
RC	Tissue=Brain;		
RC	MEDLINE=98219084; PubMed=9560155; DOI=10.1038/33416; RX		
OC	Bovinae; Bovidae; Cetartiodactyla; Ruminantia; Pecora; Bovidae; NCBI_TaxID=9913;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Fries E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nuovo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Robin G.M., Celikiner S.; Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AY058754; AAU13983_1; -.		
DR	HSSP; Q86204; IAKR.		
DR	FlyBase; FBgn0041100; park.		
DR	GO; GO:0007005; P:mitochondrion organization and biogenesis; IMP.		
RA	Minoshima S., Yokochi M., Mizuno Y., Shimizu N.;		
RT	"Mutations in the parkin gene cause autosomal recessive juvenile Parkinsonism".		
RP	Nature 392:605-608 (1998).		
RL	[2]		
DR	Smart; SM00213; UBR; 2.		
DR	SMART; SM00213; UBR; 1.		

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Om nucleic - nucleic search, using sw model

Run on:

February 25, 2005, 16:48:21 ; Search time 2103.69 Seconds

(without alignment); 10848.741 Million cell updates/sec

Title: US-10-622-817-10
Perfect score: 471

Sequence: 1 ggaagtccagcaggtagatc.....actccctgccttgtgttag 471

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
listing first 45 summaries

Database : GenEmbl:
1: gb_baa:
2: gb_htg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_patt:
7: gb_ph:
8: gb_pi:
9: gb_pr:
10: gb_ro:
11: gb_bt:
12: gb_BY:
13: gb_uu:
14: gb_vv:
15: gb_wi:
16: gb_xm:
17: gb_xn:
18: gb_xr:
19: gb_xu:
20: gb_xv:
21: gb_xw:
22: gb_xz:
23: gb_ya:
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DEFINITION	Mutations of the Parkin gene, compositions, methods and uses.			
REFERENCE	BD269536			
AUTHORS	Brice, A., Lucking, C., Abbas, N.E., Benefil, P., Ricard, S. and Bouley, S.			
COMMENT	Mutations of the Parkin gene, compositions, methods and uses			
JOURNAL	Patents; JP 200253661-A 1 05-NOV-2002;			
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PN	JP 200253661-A/1			
PD	05-NOV-2002			
PP	18-NOV-1999 JP 2000584062			
PR	19-NOV-1998 FR 98/14524, 12-MAR-1999 US 60/124239 PR 04-AUG-1999 FR 99/10140			
PI	ALEXIS BRICE, CHRISTOPHE LUCKING, NACER EDDINE ABBAS, PATRICE DENEFLÉ, RICHARD SANDRINE BOULEY			
PC	C12N15/09, A01K67/027, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/68, G01N33/15, G01N33/50, C12N15/00, C12N5/00 CC			
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Matches	468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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 Qy 121 ACCTTGACCCAGGGTCCATCTGCTGGATGATCTGAGCTTATGTTGAAAGGCCCTGT 180
 Db 359 ACCTTGACCCAGGGTCCATCTGCTGGATGATCTGAGCTTATGTTGAAAGGCCCTGT 180
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AR492172 AR492172 Sequence 1 from patent US 6716621. DNA linear PAT 15-MAY-2004

LOCUS AR492172.1 GI:47260688
 DEFINITION Sequence 1 from patent US 6716621.
 ACCESSION AR492172
 VERSION 1
 KEYWORDS
 ORGANISM Unknown
 SOURCE Unclassified.
 REFERENCE Shimizu, N. and Mizuno, Y.
 AUTHORS Isolated DNA or gene responsible for Parkinson's disease
 JOURNAL Patent: US 6716621-A 1-06-APR-2004;
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FEATURES	ORGANISM	TITLE JOURNAL
Source	Rattus norvegicus	Direct Submission (25-APR-2001) Asako Hase, Teikyo University School of Medicine, Dept. of Neurology and Neuroscience; 2-11-1, Kaga, Itabashi-ku, Tokyo 173-8605, Japan (E-mail:hase@med.teikyo-u.ac.jp), Tel:81-3-3964-1211(ex.1916), Fax:81-3-3964-6394)
FEATURES	REFERENCE	AUTHORS
Location/Qualifiers	1. Minashima, S., Shimura, H., Kubo, S., Kitada, T., Wang, M., Asakawa, S., Hattori, N., Shimura, H., Kubo, S., Kitada, T., Wang, M., Mizuno, Y., Minashima, S., Shimizu, N., Suzuki, T., Tanaka, K. and Mizuno, Y., Autosomal recessive Juvenile Parkinsonism: A key to understanding neurodegeneration in sporadic Parkinson's disease	
gene	JOURNAL	Neurobiology 20(1), 85-90 (2000)
CDS	REFERENCE	2 (bases 1 to 1564)
	AUTHORS	Hattori, N., Wang, M. and Mizuno, Y.
	TITLE	Direct Submission
	JOURNAL	Submitted (07-MAR-2000) Nobutaka Hattori, Juntendo University, Dept. of Neurology; Hongo 2-1-1, Bunkyo, Tokyo 113-8421, Japan, (E-mail:nhattori@med.juntendo.ac.jp), Tel:81-3-3813-3111(ex.3328), Fax:81-3-3813-7440)
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Query Match	96.4%; Score 454; DB 4; Length 583;	
Best Local Similarity	100.0%; Pred. No. 9,3e-138; Mismatches 0; Indels 0; Gaps 0;	
Matches	454; Conservative 0; MisMatches 0; Indel 0; Gap 0;	
Qy	1 GGAAGTCAGCAGCTAGTCACTACACAGCTTATGTTATGCCAAAGGCCCCGT	60
Db	130 GGAAGTCCAGCAGCTAGTCACTACACAGCTTATGTTATGCCAAAGGCCCCGT	189
Qy	61 CAAGAAGTCAGCAGCTAGTCACTACACAGCTTATGTTATGCCAAAGGCCCCGT	120
Db	190 CAAGAAGTCAGCAGCTAGTCACTACACAGCTTATGTTATGCCAAAGGCCCCGT	249
Qy	121 ACCTTGACCCATGGGTCATCTGCTGGGATGATGTTTAATTCACCGGATGAGTGT	180
Db	250 ACCTTGACCCAGGGTCATCTGCTGGGATGATGTTTAATTCACCGGATGAGTGT	309
Qy	181 GAATGCCAACCTCCCACACTGCCCTGGACTATGTCGAGATTTCCTTAATGGAGCA	240
Db	310 GAATGCCAACCTCCCACACTGCCCTGGACTATGTCGAGATTTCCTTAATGGAGCA	369
ORIGIN		
Query Match	75.0%; Score 353.4; DB 10; Length 1564;	
Best Local Similarity	84.8%; Pred. No. 1.4e-104; Mismatches 71; Indels 0; Gaps 0;	
Matches	396; Conservative 0; MisMatches 71; Indel 0; Gap 0;	
Db		
Qy	2 GAAGTCCAGGAGTAGATACTCACACAGCTTATGTTATGCCAAAGGCCCCGT	61
Db	301 AACATCACTTGATTAAGTGACAGAGCTGAGGCCGCTCTGGTTTCAGTCAC 360	533
Db	430 AACATCACTTGATTAAGTGACAGAGCTGAGGCCGCTCTGGTTTCAGTCAC 489	
Qy	361 TCCGGCCAGGTGTTGCTGAGCTTACACTATAGCTGTTAGCTGAGCTGAC 420	
Db	490 TCCGGCCAGGTGTTGCTGAGCTTACACTATAGCTGTTAGCTGAGCTGAC 549	
Qy	421 CGCGAGTTGTCAGGACCTCAACTTGGCTACT 454	
Db	550 CGCGAGTTGTCAGGACCTCAACTTGGCTACT 583	
RESULT 11		
AB039878	AB039878 Rattus norvegicus mRNA for Parkin, complete cds. 1564 bp linear ROD 16-APR-2004	
DEFINITION		
ACCESSION		
VERSION		
KEYWORDS		
SOURCE	Rattus norvegicus (Norway rat)	

Db	774	GGATCCCCGTGATCGCTGACCGATGTCAGGAACTCTGTCTGTCTCCATGAA	833	Db	540	GCATCCCTCGCATCCGTCACGATGTCAGGAACTCTGTCTGTCTCCATGAA	599
Qy	362	CCGCCACGTGATTGCTAGTGTCACTATACTGTGACAGACTCAATGATC	421	Qy	362	CCGCCACGTGATTGCTAGTGTCACTATACTGTGACAGACTCAATGATC	421
Db	834	ACCGCACAGTGATCTGTTGACTGTCTTCACTGTCACAGGTCACAGTC	893	Db	600	ACCGCACAGTGATCTGTTGACTGTCTTCACTGTCACAGGTCACAGTC	659
Qy	422	GCGAGTTGTACGACCTCACTTGCTACTCCCTGCGTGTG 468		Qy	422	GCGAGTTGTACGACCTCACTTGCTACTCCCTGCGTGTG 468	
Db	894	GGCAGTTGTACGACCTCACTTGCTACTCCCTGCGTGTG 940		Db	660	GGCAGTTGTACGACCTCACTTGCTACTCCCTGCGTGTG 706	
RESULT 12							
AF343575				AF343575			
DEFINITION		904 bp mRNA linear ROD 02-FEB-2002		DEFINITION			
ACCESSION		Rattus norvegicus parkin transcript variant 7 mRNA, complete cds.		ACCESSION			
VERSION		AF343575.1 GI:18478869		VERSION			
KEYWORDS				KEYWORDS			
SOURCE				SOURCE			
ORGANISM		Rattus norvegicus (Norway rat)		ORGANISM			
REFERENCE				REFERENCE			
AUTHORS		D'Agata,V.M., Scapagnini,G. and Cavallaro,S.		AUTHORS			
TITLE		Functional and molecular diversity of parkin in the rat brain		TITLE			
JOURNAL		Unpublished		JOURNAL			
REFERENCE		2 (bases 1 to 904)		REFERENCE			
AUTHORS		D'Agata,V.M., Scapagnini,G. and Cavallaro,S.		AUTHORS			
TITLE		Direct Submission		TITLE			
JOURNAL		Submitted (29-JAN-2001) Institute of Biointaging and Pathophysiology (CRN), Piazza Roma, 2, Catania 95123, Italy		JOURNAL			
FEATURES				FEATURES			
source		Location/Qualifiers		source			
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		/mol_type="mRNA"					
CDS		/db_xref="taxon:10116"		CDS			
		410-.745 /codon_start=1					
		/product="parkin transcript variant 7"					
		/protein_id="P417349.1"					
		/do_xref="GI:18478870"					
		/translation="MSGCQSPUPGTRAFFKGAHPTSDTSVALNLITNSRSIPCIACTVRNPVILVFOCNHRHVICLDCFHLIVCUTRLNDRQFVHDALQYSLPCVVRFLGQLQGSIP"					
ORIGIN				ORIGIN			
Query Match		74.4%; Score 350.2; DB 10; Length 904;		Query Match		74.0%; Score 348.6; DB 10; Length 1466;	
Best Local Similarity		84.4%; Pred. No. 1.5e-103; Mismatches 394; Conservative 0; Indels 0; Gaps 0;		Best Local Similarity		84.2%; Pred. No. 5.3e-103; Mismatches 393; Conservative 0; Indels 0; Gaps 0;	
Matches				Matches			
Qy	2	GAAGTCAGGAGGTAGATCACTACAACGCTTATGCTGTTAATGCAAGGCCCTGC	61	Qy	2	GAAGTCAGGAGGTAGATCACTACAACGCTTATGCTGTTAATGCAAGGCCCTGC	61
Db	240	AGGTCAGGAGCTAACCAACCACTACACAGCTTCTGCAAGGAACTGCTGCC	299	Db	494	GAGTCAGGAGCTAACCAACCACTACACAGCTTCTGCAAGGAACTGCTGCC	553
Qy	62	AAAGAGTGCAGGCCGAAACTCAGGTAGTCAGCAGAACCTGAGGGGGAAAGCTCA	121	Qy	62	AAAGAGTGCAGGCCGAAACTCAGGTAGTCAGCAGAACCTGAGGGGGAAAGCTCA	121
Db	300	ACAGGTCCAGCTGGAAACTCCGAGTCAGTCAGTCAGGCAACCTGAGCAACCTCA	359	Db	554	ACAGGTCCAGCTGGAAACTCCGAGTCAGTCAGGCAACCTGAGCAACCTCA	613
Qy	122	CCTGACCCGGGTCATCTGCTGGATGAGTCTTAATCCAAACGGGAGTAGTGTG	181	Qy	122	CCTGACCCGGGTCATCTGCTGGATGAGTCTTAATCCAAACGGGAGTAGTGTG	181
Db	360	CCTGACCCGGGTCATCTGCTGGATGAGTCTTAATCCAAACGGGAGTAGTGTG	419	Db	614	CCTGACCCGGGTCATCTGCTGGATGAGTCTTAATCCAAACGGGAGTAGTGTG	673
Qy	182	ATGCCAACTCCCACACTGCCCTGGACTAGTCAGAATTTCTTAATGAGGACAC	241	Qy	182	ATGCCAACTCCCACACTGCCCTGGACTAGTCAGAATTTCTTAATGAGGACAC	241
Db	420	AGTCCAACTCCAGACTCCCTGGACAGGTGAATTCTTAAATGAGGACAC	479	Db	420	AGTCCAACTCCAGACTCCCTGGACAGGTGAATTCTTAAATGAGGACAC	479
Qy	242	ACCCACCTCTGACAGAACATCAGTGTGACCTGTGACAAATAGTGTG	301	Qy	242	ACCCACCTCTGACAGAACATCAGTGTGACCTGTGACAAATAGTGTG	301
Db	480	ACCCACCTCTGACAGAACATCAGTGTGACCTGTGACAAACAGCCCA	539	Db	554	ACCCACCTCTGACAGAACATCAGTGTGACCTGTGACAAACAGCCCA	613
Qy	302	ACATCACTGCACTACGTCACAGCAGGCTAGGACCCGCTCTGTTTCACTGCACT	361	Qy	302	ACATCACTGCACTACGTCACAGCAGGCTAGGACCCGCTCTGTTTCACTGCACT	361

OY	182	ATGCCAATCCCAACTGCCCTGGACTTAGTGAGATTCTTAAATGGGAGAC	241	Db	466	GAGGTCCAGAGCTAACCCACCTACCAAGCTTTGTCAGTCAGAAGGCCCTGCC	525
Db	674	AGTCCAACTCCAGACTCCCTGGACAGAGGTGAAATTCTTAATGGAGAC	733	OY	62	AAAGAGTGCAGCGGGAAACTCAGGGTACAGTGAGACCTGGAGGCAAGCTCA	121
OY	242	ACCCACCTCTGACAAGGAAACATCAGTAGCTTGCACAAATAGTCGA	301	Db	526	AACAGGTCTAGCTGGAACTCGGAGTCAGTGGGAACTCGAGAAGAACCTCA	585
Db	734	ACCCACCTCTGACAAGGAAACATCAGTAGCTTGCACAAATAGTCGA	733	OY	122	CCTGACCOAGGGTCATCTGCTGGATGATGTTAATCCAACCGATGAGTGTG	181
OY	302	ACATCACTGCAATTAGGCAAGAGTCAGGAGCCGTCCTGGATCAGTCGA	361	Db	586	CCTGGCCAGGSCCACTCTGGAGATGTCCTAACTCCAAACGGATGAGTGTG	645
Db	794	GCATCCCTGCACTGGCACTGGGACTAGTCAGTGGACTTAGTCAGA	853	OY	182	AATGCCAATCCCAACTGCCCTGGACTAGTCAGAAGCTAAATGAGCAC	241
OY	362	CCCCCACCTGATTGCTTAGCTTCCACTATACGTGACAGACTCAATGATC	421	Db	646	AGTCCAACTCCAGACTGCCCTGGACAGAGGTGAGAC	705
Db	854	ACCCACCTGATCTGGTGGACTGCTTCACCTGACTGTGTCACAGGCTAAC	913	OY	242	ACCCACCTGACAAGGAAACATCAGTAGCTTGCACAAATAGTCGA	301
OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468	Db	706	ACCCACCTGACAAGGAAACATCAGTAGCTTGCACAAATAGTCGA	765
Db	914	GCGAGTTGTCACGACGCTACGTGGCTACGGTGGTGTG	960	OY	302	ACATCACTGCAATTAGGCAAGAGTCAGTGGACTAGTCAGAAGCTAAATGAGCAC	361
RESULT 14							
LOCUS	AF210434	1576 bp mRNA linear	ROD 02-JUL-2002	Db	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	825
DEFINITION	Rattus norvegicus parkin mRNA, complete cds.			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
ACCESSION	AF210434			OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
VERSION	AF210434.1			Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
KEYWORDS				OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
SOURCE				Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
ORGANISM	Rattus norvegicus (Norway rat)			OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
REFERENCE	1. (bases 1 to 1576)			Db	766	GCATCCCTGCACTGGACAGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	765
AUTHORS	Gu, W.J., Abbas, N.E.			OY	766	GCATCCCTGCACTGGACAGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	765
TITLE	Direct Submission			Db	766	GCATCCCTGCACTGGACAGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	765
JOURNAL	Submitted (02-DIC-1999) Neurology, INSERM U289, 47, Boulevard de L'Hopital, Paris 75013, France			OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	825
FEATURES	source			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
REFERENCE	1. (bases 1 to 1576)			OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
AUTHORS	/organism="Rattus norvegicus"			Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
MOL_TYPE	/mol_type="mRNA"			OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
DB_XREF	/db_xref="taxon:10116"			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
TISSUE_TYPE	/tissue_type="hypothalamus"			OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
CDOS	63. .1460			Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
REFERENCE	/codon_start=1			OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
AUTHORS	/product="parkin"			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
TITLE	/protein_id="AAQ37013.1"			OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
JOURNAL	/db_xref="GI:1157824"			Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
FEATURES	source			OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
REFERENCE	1. (bases 1 to 1157)			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
AUTHORS	D'Agata, V.M., Scapagnini, G. and Cavallaro, S.			OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
TITLE	Functional and molecular diversity of Parkin in the rat brain			Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
JOURNAL	Unpublished			OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
REFERENCE	2. (bases 1 to 1157)			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
AUTHORS	D'Agata, V.M., Scapagnini, G. and Cavallaro, S.			OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
TITLE	Functional and molecular diversity of Parkin in the rat brain			Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
JOURNAL	(CNR), Pizza Roma, 2, Catania 95123, Italy			OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
FEATURES	location/Qualifiers			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
REFERENCE	1. .1157			OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
AUTHORS	/product="Parkin transcript variant 6"			Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
TITLE	/codon_start=1			OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
JOURNAL	/product="Parkin transcript variant 6"			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
FEATURES	source			OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
REFERENCE	1. .1157			Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
AUTHORS	/organism="Rattus norvegicus"			OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
MOL_TYPE	/mol_type="mRNA"			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
DB_XREF	/db_xref="axon:10116"			OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
TISSUE_TYPE				Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
CDOS				OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
REFERENCE	333. .1157			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
AUTHORS				OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
TITLE				Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
JOURNAL				OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
FEATURES	location/Qualifiers			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
REFERENCE	1. .1157			OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
AUTHORS	/product="Parkin transcript variant 6"			Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
TITLE	/codon_start=1			OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
JOURNAL	/product="Parkin transcript variant 6"			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
FEATURES	source			OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
REFERENCE	1. .1157			Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
AUTHORS	/organism="Rattus norvegicus"			OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
MOL_TYPE	/mol_type="mRNA"			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
DB_XREF	/db_xref="axon:10116"			OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
TISSUE_TYPE				Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
CDOS				OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
REFERENCE	333. .1157			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
AUTHORS				OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
TITLE				Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
JOURNAL				OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
FEATURES	location/Qualifiers			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
REFERENCE	1. .1157			OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
AUTHORS	/product="Parkin transcript variant 6"			Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
TITLE	/codon_start=1			OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
JOURNAL	/product="Parkin transcript variant 6"			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
FEATURES	source			OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
REFERENCE	1. .1157			Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
AUTHORS	/organism="Rattus norvegicus"			OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
MOL_TYPE	/mol_type="mRNA"			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
DB_XREF	/db_xref="axon:10116"			OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
TISSUE_TYPE				Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
CDOS				OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
REFERENCE	333. .1157			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
AUTHORS				OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
TITLE				Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
JOURNAL				OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
FEATURES	location/Qualifiers			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
REFERENCE	1. .1157			OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
AUTHORS	/product="Parkin transcript variant 6"			Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
TITLE	/codon_start=1			OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
JOURNAL	/product="Parkin transcript variant 6"			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
FEATURES	source			OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
REFERENCE	1. .1157			Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
AUTHORS	/organism="Rattus norvegicus"			OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
MOL_TYPE	/mol_type="mRNA"			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
DB_XREF	/db_xref="axon:10116"			OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
TISSUE_TYPE				Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
CDOS				OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
REFERENCE	333. .1157			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
AUTHORS				OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
TITLE				Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
JOURNAL				OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
FEATURES	location/Qualifiers			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
REFERENCE	1. .1157			OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
AUTHORS	/product="Parkin transcript variant 6"			Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
TITLE	/codon_start=1			OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
JOURNAL	/product="Parkin transcript variant 6"			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
FEATURES	source			OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
REFERENCE	1. .1157			Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
AUTHORS	/organism="Rattus norvegicus"			OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
MOL_TYPE	/mol_type="mRNA"			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
DB_XREF	/db_xref="axon:10116"			OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
TISSUE_TYPE				Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
CDOS				OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
REFERENCE	333. .1157			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
AUTHORS				OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
TITLE				Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
JOURNAL				OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
FEATURES	location/Qualifiers			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	885
REFERENCE	1. .1157			OY	422	GGAATGTTTACGACGCCACTTGCTCATCCCTGCCTGTGTG	468
AUTHORS	/product="Parkin transcript variant 6"			Db	886	GCGAGTTGTCACGACGCTACGTGGACTAGTCAGTGTGAGCTACCAACAGCCCA	932
TITLE	/codon_start=1			OY	362	CCCCCACTGATGTTGCTTAGCTTGCACAGTCAGGAGCCGTCCTGGTCTCCANTGTAACC	421
JOURNAL	/product="Parkin transcript variant 6"			Db	826	ACCCACCTGATGTTGCTTAGCTTGCACAGTCAGGAGCC	

Matches	392; conservative	0;	Mismatches	73;	Indels	0;	Gaps	0;
Ov	4	AGTCAGGAGTAGATCAATCTACAAACAGCTTATGTTGATGTTGCAAAAGCCCTGTAA		63				
Db	165	AATCACGGACTAAACCCACCTTACACAGCTTGTCTACTCGAACAGCCCTGCCAC						224
Ov	64	AGATGCGACGGGAAACTCAAGCTACGTTGAGCTGGCAGCGAACGCTAAC		123				
Db	225	AATGTCAGCTGGAAACTCCGAGTTCAAGCTACCGAACCTCACC						284
Ov	124	TGAAACCGGGTCACTTGCTGGATGATGTTTAATCCAAACGGATGAGTGGGA		183				
Db	285	TGCCCCAGGGCCATCTGCTGGATGATGCTTAATTCCAAACGGATGAGTGGAG						344
Ov	184	TGCATACTCCCACACTGCGCTGGACTACTGCGAATTTCTTTAAATGGAGCAC		243				
Db	345	TGCCAATCTCCAGACTGCCCTGGACAAGAGCTGAAATTCTTAATGGAGCAC						404
Ov	244	CCCACCTCTGACAGGAAACATCAGTACCTTGACCTTGATGCCAACAAATGCTGGAC		303				
Db	405	CACACCTCAGACAGGACACATCAGTACCTTGACCTTGATGCCAACAAATGCTGGAC						464
Ov	304	ATCCTTGATTAAGTGCACAGAGCTCAGGAGCCGCTCTGGTTCCAGTGAACTCC		363				
Db	465	ATCCCTGCACTCGCTGACAGGAGCTGGCTTGTCTCCAAATGTAACAC						524
Ov	364	GGCACCGTGTATCTCTTACGTGTTCCACTTAACTTACTGTTGAGACATCTAATGATCG		423				
Db	525	GGCACCGTGTATCTCTTACGTGTTGACTGCTTCACTGTGACTGTGACAAAGCTAACGATCG						584
Ov	424	CAGTTGTCACACCCCTCACTGGTACTCTCCACCTTGTTG 468						
Db	585	CAGTTGTCACACGGCTCAGCTTGCTACTCGCTGCCGIGTG 629						

Search completed: February 26, 2005, 02:12:59
 Job time : 2105.69 secs

Run on: February 25, 2005, 15:46:49 ; Search time 265.776 Second
 (without alignments)
 10490.795 Million cell updates/sec

Title: Om nucleic - nucleic search, using bw model

Perfect score: US-10-622-817-10

Sequence: 1 gaaagtccagcaggtagatc.....actccatgttttgtttag 471

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database	No.	Score	Query Length	DB ID	Description
N_Geneseq_16Dec04:*	1:	geneseqn1980B:*			
2:	471	100.0	471	5 AAH77664	Anh77664 Nucleotid
3:	468	99.4	2960	3 AAA6765	Ana46765 cDNA sequ
4:	466.4	99.0	2960	2 AAH99923	Anx99923 Human par
5:	466.4	99.0	2960	8 ADD7679	And7679 Human Par
6:	466.4	99.0	2960	8 ADD47680	And47680 Human Par
7:	340.2	72.2	3043	4 AAF55253	And1332 Human DNA
8:	340.2	72.2	3092	4 AAF55257	Aat55253 Nucleotid
9:	340.2	72.2	3253	4 AAF55256	Aaf55256 Nucleotid
10:	340.2	72.2	3253	4 AAF55254	Aaf55254 Nucleotid
11:	340.2	72.2	3254	4 AAF55255	Aaf55255 Nucleotid
12:	340.2	72.2	3255	4 AAF55259	Aaf55259 Nucleotid
13:	340.2	72.2	3255	4 AAF55244	Aaf55244 Nucleotid
14:	340.2	72.2	3256	4 AAF55260	Aaf55260 Nucleotid
15:	340.2	72.2	3255	4 AAF55258	Aaf55258 Nucleotid
16:	338.6	71.9	3014	4 AAF55247	Aaf55247 Nucleotid
17:	288.4	61.2	2876	2 AAX9924	Aax9924 Human par
18:	288.4	61.2	2076	8 ACD1333	Acd1333 Human DNA
19:	265.4	56.3	3186	4 AAF55250	Aaf55250 Nucleotid
20:	262.8	55.8	2893	4 AAF55248	Aaf55248 Nucleotid

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	471	100.0	471	5 AAH77664
2	468	99.4	2960	3 AAA6765
3	466.4	99.0	2960	2 AAH99923
4	466.4	99.0	2960	8 ADD7679
5	466.4	99.0	2960	8 ADD47680
6	466.4	99.0	2960	8 ACD1332
7	340.2	72.2	3043	4 AAF55253
8	340.2	72.2	3092	4 AAF55257
9	340.2	72.2	3253	4 AAF55256
10	340.2	72.2	3253	4 AAF55254
11	340.2	72.2	3254	4 AAF55255
12	340.2	72.2	3255	4 AAF55259
13	340.2	72.2	3255	4 AAF55244
14	340.2	72.2	3256	4 AAF55260
15	340.2	72.2	3255	4 AAF55258
16	338.6	71.9	3014	4 AAF55247
17	288.4	61.2	2876	2 AAX9924
18:	288.4	61.2	2076	8 ACD1333
19:	265.4	56.3	3186	4 AAF55250
20:	262.8	55.8	2893	4 AAF55248

RESULT 1

ID AAH77664 standard; DNA; 471 BP.

XX AAH77664;

AC XX

DT 13-NOV-2001 (first entry)

XX DE Nucleotide sequence of human Parkin protein fragment.

XX KW Human; Parkin-Associated Protein 1; Papi; Parkin gene; neurodegenerative disease; Parkinson's disease; ss.

XX OS Homo sapiens.

XX PN WO200160857-A2.

XX PD 23-AUG-2001.

XX PF 15-FEB-2001; 2001WO-FR000461.

XX PR 17-FEB-2000; 2000FR-00001980.

XX PR 18-APR-2000; 2000US-0198489P.

PA (AVET) AVENTIS PHARMA SA.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX PI Koutnikova H, Brice A, Fournier A, Pradier L, Prades C; Arnould-Reigngne I, Rosier-Montus M, Corti O;

XX PI Arnould-Reigngne I, Rosier-Montus M, Corti O;

XX DR WPI: 2001-550047/61.

DR P-PSDB; AAG67213.

XX PT A new protein, designated Parkin-Associated Protein 1 (PAPI), is an interaction partner of Parkin and is useful to treat neurodegenerative pathologies including Parkinson's disease.

XX PS Example 1, Page 60-61; 82pp; French.

CC The present sequence encodes the central region of a human Parkin protein. The protein was used to identify Parkin-Associated Protein 1 (PAPI) protein. PAPI is associated with the Parkin gene, which is mutated in certain forms of familial (juvenile autosomal recessive) Parkinson's

CC disease. PAP1 has some homology with synaptotagmins. PAP1 is used to treat neurodegenerative diseases, particularly to diagnose and treat Parkinson's disease.

XX Sequence 471 BP; 118 A; 127 C; 109 G; 117 T; 0 U; 0 Other;

Query Match 100.0%; Score 471; DB 5; Length 471;
Best Local Similarity 100.0%; Pred. No. 7.8e-153; PT
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Ov 1 GGAGTCAGCAGGTTAGTCACTACACGCTTATGGTATGCAAAGGCCCTGT
Db 61 CAAGAGTGCAGCCGGAAACTCAGGGTAGTGTGAGCACCTGCAGGAGGAAACGCTC 60
Qy 61 CAAGAGTGCAGCCGGAAACTCAGGGTAGTGTGAGCACCTGCAGGAGGAAACGCTC 60
Db 61 CAAGAGTGCAGCCGGAAACTCAGGGTAGTGTGAGCACCTGCAGGAGGAAACGCTC 120
Qy 121 ACCTTGACCCAGGTCACTGCTGGATGATGTTTAATGAGGAGCA 180
Db 121 ACCTTGACCCAGGTCACTGCTGGATGATGTTTAATGAGGAGCA 180
Qy 181 GATGCGAACATCCACACTGCGCTGGACTGTCGAATTTCCTTAATGAGGAGCA 240
Db 181 GATGCGAACATCCACACTGCGCTGGACTGTCGAATTTCCTTAATGAGGAGCA 240
Qy 241 ACCCGACTCTGACAGGAAACATCAGTACCTTGACCTGACCGTATGCGAACAACTAGTCG 300
Db 241 GACCCACCTCTGACAGGAAACATCAGTACCTTGACCTGACCGTATGCGAACAACTAGTCG 300
Qy 301 AACATCACTTGATGAGCTTGACAGGAGCCCTCCCTGGTTTCAGTCAC 360
Db 301 AACATCACTTGATGAGCTTGACAGGAGCCCTCCCTGGTTTCAGTCAC 360
Qy 361 TOCCGCCACGTTGATGTTTCACTTATCTGTTGACAGAATCAATG 420
Db 361 TOCCGCCACGTTGATGTTTCACTTATCTGTTGACAGAATCAATG 420
Qy 421 CGGCAGTTGTCAGACCCCTAACTTGGCTCTGTTGAGCTTCACTTATCTGTTGAG 471
Db 421 CGGCAGTTGTCAGACCCCTAACTTGGCTCTGTTGAGCTTCACTTATCTGTTGAG 471

RESULT 2

AAA46765 ID AAA46765 standard; cDNA; 2960 BP.
XX AC AAA46765;
XX DT 25-SEP-2000 (first entry)
DB CDNA sequence of the human parkin protein gene.
XX Human; parkin protein; parkin gene; Parkinson's disease; anti-Parkinson agent; ss. OX Homo sapiens.
XX OS Homo sapiens.
XX PN WO20031253-A2.
XX PD 02-JUN-2000.
XX PF 18-NOV-1999; 99WO-FR002833.
XX PR 19-NOV-1998; 98FR-00014524.
PR 12-MAR-1999; 99US-0124235P.
PR 04-AUG-1999; 99FR-00010140.
XX PA (RHON) RHONE-POULENC RORER SA.
PA (INRM) INST NAT SANTE & RECH MEDICALE.
XX PI Brice A, Lucking C, Abbas NE, Denefle P, Ricard S, Bouley S;
XX

RESULT 3

AAX99923 ID AAX99923 standard; DNA; 2960 BP.
XX AC AAX99923;
XX DT 21-OCT-1999 (first entry)
XX DE Human parkin gene variant.
XX KW Parkinson's disease related gene; parkin gene; variant; gene therapy; ss.
OS Homo sapiens.
XX FH Key CDS Location/Qualifiers
FT 102. 1499

DR WPI; 2000-411952/35.
XX
PT New variant form of the human Parkin gene, used as source of primers and probes for detecting susceptibility to Parkinson's disease.
XX PS Claim 24; Fig 1; 71pp; French.
XX The present sequence represents a cDNA sequence of the human parkin protein gene. The specification describes a parkin gene which has genetic alterations. Cells, or transgenic animals, that express the altered parkin gene are used to screen for compounds that can counter the effects of a genetic alteration in the parkin gene, or more generally for studying the properties of the parkin protein. Detection of the specified alterations is used to diagnose susceptibility to Parkinson's disease. The modified polynucleotide is also used to express the corresponding protein, which is then used to screen for potential anti-Parkinson agents and to raise antibodies (for detecting variants of parkin protein).

XX Sequence 2960 BP; 815 A; 726 C; 698 G; 721 T; 0 U; 0 Other;
Best Local Similarity 100.0%; Pred. No. 2.3e-151; PT
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Ov 1 GGAGTCAGCAGGTTAGTCACTACACGCTTATGGTATGCAAAGGCCCTGT 60
Db 504 GGAGTCAGCAGGTTAGTCACTACACGCTTATGGTATGCAAAGGCCCTGT 563
Qy 61 CAAGAGTGCAGCCGGAAACTCAGGGTAGTGTGAGCACCTGCAGCACCTGCAGGAGGAAACGCTC 120
Db 564 CAAGAGTGCAGCCGGAAACTCAGGGTAGTGTGAGCACCTGCAGCACCTGCAGGAGGAAACGCTC 623
Qy 121 ACCTTGACCCAGGTCACTGCGCTGGACTGTCGAATTTCCTTAATGAGGAGCA 180
Db 624 ACCTTGACCCAGGTCACTGCGCTGGACTGTCGAATTTCCTTAATGAGGAGCA 743
Qy 181 GATGCGAACATCCACACTGCGCTGGACTGTCGAATTTCCTTAATGAGGAGCA 240
Db 684 GATGCGAACATCCACACTGCGCTGGACTGTCGAATTTCCTTAATGAGGAGCA 743
Qy 241 GACCCACCTTGACAGGAAACATCAGTACCTTGACCTGACAGAATCAATG 300
Db 744 CACCCACCTTGACAGGAAACATCAGTACCTTGACCTGACAGAATCAATG 803
Qy 301 AACATCACTTGATGAGCTTGACAGGAGCCCTCCCTGGTTTCAGTCAC 360
Db 804 AACATCACTTGATGAGCTTGACAGGAGCCCTCCCTGGTTTCAGTCAC 863
Qy 361 TOCCGCCACGTTGATGTTTCACTTATCTGTTGACAGAATCAATG 420
Db 864 TOCCGCCACGTTGATGTTTCACTTATCTGTTGACAGAATCAATG 923
Qy 421 CGGCAGTTGTCAGACCCCTAACTTGGCTCTGTTGAGCTTCACTTATCTGTTGAG 468
Db 924 CGGCAGTTGTCAGACCCCTAACTTGGCTCTGTTGAGCTTCACTTATCTGTTGAG 971

/*tag= a

FT XX WO9940191-A1.
XX PN DE Human Parkin protein encoding cDNA.
PD 12-AUG-1999.
XX KW Human; Parkin protein; neurological disorder; apoptosis; gene therapy;
KW ischaemic stroke; Parkinson's disease; nootropic;
KW transgenic; cerebroprotective; neuroprotective; neurotransplantation;
KW gene; ss.
XX PA (SHIM/) SHIMIZU N.
PA (NIZU/) MIZUNO Y.
XX PT Shimizu N, Mizuno Y;
XX PI XX WPI; 1999-494295/41.
DR DR P-PSDB; AAY32501.

PT Gene implicated in the pathology of Parkinson's disease, used for
PT treatment of the disease.
XX

PS Claim 1; Page 83-88; 114pp; English.

CC This sequence represents a gene of the invention, and is implicated in
the pathology of Parkinson's disease. This sequence is a variant of the
parkin gene found in Parkinson's disease patients. The sequences may be
used for the diagnosis, treatment (including gene therapy) and
CC investigation of Parkinson's disease

XX Sequence 2960 BP; 815 A; 727 C; 698 G; 720 T; 0 U; 0 Other;

SQ Query Match 99.0%; Score 466.4; DB 2; Length 2960;
Best Local Similarity 99.8%; Pred. No. 8.4e-151;
Matches 467; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Ov 1 GGAAGTCAGCAGGCTAGATCATCTACACAGCTTATGTGATTTGAGGAAAGGCCCTG 60
Db 504 GGAGAGTCAGCAGGCTAGATCATCTACACAGCTTATGTGATTTGAGGAAAGGCCCTG 563

Ov 61 CAAGAGTCAGCAGGCTAACATCAGGGTACAGTGAGCACTCGAGACTCGAGGAGAACGCTC 120
Db 564 CAAGAGTCAGCAGGCTAACATCAGGGTACAGTGAGCACTCGAGACTCGAGGAGAACGCTC 623

Ov 121 ACCTTGACCCAGGGTCATCTGCTGGATGATGTTTAATTCAAACGGATGAGTGT 180
Db 624 ACCTTGACCCAGGGTCATCTGCTGGATGATGTTTAATTCAAACGGATGAGTGT 683

Ov 181 GAATGCCAATCCCAACTGCCCCTGGACTAGTCGAGATTTCCTTAATGPGACCA 240
Db 684 GAATGCCAATCCCAACTGCCCCTGGACTAGTCGAGATTTCCTTAATGPGACCA 743

Ov 241 CACCCCACCTTGACAGGAAACATCAGTAGCTTGACCTGATCGAACAAATAGTCG 300
Db 744 CACCCCACCTTGACAGGAAACATCAGTAGCTTGACCTGATCGAACAAATAGTCG 803

Ov 301 AACATCACTTGATTAAGTGACAGGCTTGACAGGCTTGACCTGATCGAACAAATAGTCG 360
Db 804 AACATCACTTGATTAAGTGACAGGCTTGACCTGATCGAACAAATAGTCG 863

Ov 361 TCCGGCCAGCTGATAGTCGACAGGCTTGACCTGATCGAACAAATAGTCG 420
Db 864 TCCGGCCAGCTGATAGTCGACAGGCTTGACCTGATCGAACAAATAGTCG 923

Ov 421 CGCGAGTTGTCAGACCTCAACTTGCTACTCCCTGCTTGCTG 468
Db 924 CGCGAGTTGTCAGACCTCAACTTGCTACTCCCTGCTTGCTG 971

RESULT 4 ADD47679 ID ADD47679 XX AC ADD47679;

XX DR DR P-PSDB; AAE30800.

XX PT New isolated nucleic acid sequence encoding a Parkin polypeptide, useful
PT for treating, preventing or diagnosing neurological disorders, e.g.
PT Parkinson's disease, Alzheimer's disease or ischemic stroke, and in
PT screening assays.

PS Example 1; Page 68-69; 71pp; English.

XX The invention relates to Parkin protein and its corresponding nucleic
CC acid sequence. The nucleic acid sequence is useful for altering the
CC proteolytic processing of Parkin at its potential cleavage site at Asp
CC 126. The invention is used in manufacturing or testing a pharmaceutical
CC composition for treating and/or preventing a neurological disorder, e.g.
CC Alzheimer's disease or ischaemic stroke. It also used for detecting the
CC occurrence of proteolytic processing of Parkin at Asp 126 in a sample, in
CC monitoring a potential disposition for a neurodegenerative disease, and
CC for treating, preventing and/or diagnosing Parkinson's disease or other
CC neurodegenerative disorders. The viral vector is used for transforming
CC neuronal cells in vivo or ex vivo. The invention is useful for
CC neurotransplantation into the CNS of a mammal. It may be used in
CC screening assays to identify compounds that increase or decrease
CC apoptosis. It is also used in gene therapy. The present sequence is human
CC Parkin protein encoding cDNA

XX Sequence 2960 BP; 815 A; 727 C; 698 G; 720 T; 0 U; 0 Other;

SQ Query Match 99.0%; Score 466.4; DB 8; Length 2960;
Best Local Similarity 99.8%; Pred. No. 8.4e-151;
Matches 467; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Ov 1 GGAAGTCAGCAGGCTAGATCATCTACACAGCTTATGTGATTTGAGGAAAGGCCCTG 60
Db 504 GGAGAGTCAGCAGGCTAGATCATCTACACAGCTTATGTGATTTGAGGAAAGGCCCTG 563

Ov 61 CAAGAGTCAGCAGGAAACATCAGGGTACAGTGAGCACTCGAGACTCGAGGAGAACGCTC 120
Db 564 CAAGAGTCAGCAGGAAACATCAGGGTACAGTGAGCACTCGAGACTCGAGGAGAACGCTC 623

Ov 121 ACCTTGACCCAGGGTCATCTGCTGGATGATGTTTAATTCAAACGGATGAGTGT 180
Db 624 ACCTTGACCCAGGGTCATCTGCTGGATGATGTTTAATTCAAACGGATGAGTGT 683

XX
 PR 05-JUN-2001; 2001US-0296076P.
 PR 10-OCT-2001; 2001US-0388605P.
 PR 15-FEB-2002; 2002US-0357725P.
 PA
 XX Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
 PI XX WPI; 2003-156859/15.
 DR XX P-PSDB; ABO07156.
 PT XX Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53 pathway in *Drosophila*.
 PT XX
 PS XX Example 2: Page 166-167, 678bp; English.
 The invention relates to identifying (M1) a candidate p53 pathway modulating agent, by contacting an assay system comprising a purified HM polypeptide (human orthologue of genes that modify the p53 pathway in *Drosophila*) or nucleic acid with a test agent under conditions, where but for the presence of the test agent, the system provides a reference activity, and detecting a test agent-biased activity of the assay system. Also included are modulating (M2) a p53 pathway of a cell (comprising contacting a cell defective in p53 function with a candidate modulator that specifically binds to a HM polypeptide comprising an HM amino acid sequence, where p53 function is restored), modulating (M3) a p53 pathway in a mammalian cell (comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with a probe for HM expression; (c) comparing the results with a control; and (d) determining whether the comparison indicates a likelihood disease). (M1) is useful for identifying modulators of the p53 pathway. A probe for HM expression is useful for diagnosing breast, colon, kidney, lung and ovarian cancer. Modulators identified by (M1) are useful in a variety of diagnostic and therapeutic applications, where disease or disorder prognosis is related to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell proliferation disorders (e.g. cancer). Another two new methods (M2 and M3) are useful for modulating the p53 pathway of a cell, thus restoring the p53 function of the cell, so that the cell undergoes normal proliferation or progression through the cell cycle. (M2) and (M3) are also useful for treating defects in the p53 pathway such as, angiogenic, apoptotic or cell proliferation disorders. The present sequence is an HM nucleic acid encoding a p53 pathway modifying protein
 XX SQ Sequence 2960 BP; 815 A; 727 C; 698 G; 720 T; 0 U; 0 Other;
 Query Match 99.0%; Score 466.4; DB 8; Length 2960;
 Best Local Similarity 99.8%; Pred. No. 8.4e-151;
 Matches 467; Conservative 0; Mismatches 1; Indels 0; Gaps 0
 Oy 1 GGAAAGTCCAGCAGGATGATCATCTACACAGCTTTATGTTATTCAGGCCCTGT 60
 Db 504 GGAAAGTCCAGCAGGATGATCATCTACACAGCTTTATGTTATTCAGGCCCTGT 563
 Oy 61 CAAGAGACTGAGCCGGAAGACTCGGGTAGTGCAGCTGACACTGCAACGCTC 120
 Db 564 CAAGAGACTGAGCCGGAAGACTCGGGTAGTGCAGCTGACACTGCAACGCTC 623
 Oy 121 ACCTTGACCGAGGTGACATCTGCTGGATGATGTTTAATCCAAACGGATGAGCTG 1800
 Db 624 ACCTTGACCGAGGTGACATCTGCTGGATGATGTTTAATCCAAACGGATGAGCTG 683
 Oy 181 GAATGCCAATCCCAACTGCGCTGGACTGTGCAAGATTCTTAAATGTGGAGCA 2400
 Db 684 GAATGCCAATCCCAACTGCGCTGGACTGTGCAAGATTCTTAAATGTGGAGCA 743
 Oy 241 CACCCACCTGAGAAGGAAACATGAGTAGCTTGTGCGCTTGTGCGCTTGTGCGG 3000

Sequence	3043	Score	340.2;	DB	4;	Length	3043;	SQ
Best Local Similarity	84.0%;	Pred.	No.	7e-107;				DR
Matches	384;	Conservative	0;	Mismatches	73;	Indels	0;	p-PSDB;
Qy	11	CUGGTAGATCACTACACACTTGTGATGTTGATGCCAAGCCCCGTGCAAGAGTGCC	70	PT	New poly nucleotides encoding mouse parkin2 protein, useful for producing			
	538	CAGTTAACCCACCTACACAGCTTTCATCTACTCAAAAGGCCCGGCCACAAGGTC	597	PT	a transgenic non-human animal as an animal model for neurodegenerative			
	Db	71 AGCGGGAAACTCGAGTAGCTGAGCTGAGCAGCGAACGCTCACCTGACCC	130	PT	diseases.			
	Qy	131 AGGGTCACTCTGCTCGAGTGTGTTAATCCAAACGGATGAGGTTGATGCAAT	190	PT				
	Db	598 AGGCTGAAAGCTCCAGTCACTGAGTCAGTGCAGCTGAGCACCTGCAACACCTGCCC	657	PT				
	Qy	191 CCCCAACTGCGTGGACTAGTGCAGAATTTCCTTAATGCGAGCACCCACT	250	CC	Parkinson's disease in humans. The human parkin2 gene is located in gene			
	Db	718 CTCCACAGCATAGTAGTTGCGACCGAGCTGAAATTCTTAATGCGAGCACCAACT	777	CC	region 6q25.2-27. Parkin2 polypeptides and poly nucleotides are useful for			
	Qy	251 CTGACAGGAACTGCGCTGCAGACAGCTGAGCTGAAATTCTTAATGCGAGCACCAACT	310	CC	analysing neurodegenerative diseases. They are also useful for testing			
	Db	778 CAGACAGGACGCTGCTGAGCTGTTGACCTGATCACCGAACAGCGAGCATCCT	837	CC	the efficacy of the treatment of a neurodegenerative disease such as			
	Qy	311 GCATTACGTGCAAGAGCTGAGGAGCCGCGCTGCTGAGTCAACTCCCGACG	370	CC	Parkinson's disease, Alzheimer's disease, Huntington's disease,			
	Db	838 GCATAGCGTGCAAGATGCTCAGGAGCGCTGCTGAGCTAACCGCTCAGG	897	CC	Pick's disease, Prion disease, and secondary causes inducing Parkinson's			
	Qy	371 TGATTGCTGACTGTTTCACTTAATCTGTCAGAAGCTCAATGATGGAGTTG	430	CC	syndromes like toxins, drugs, brain tumours, head trauma, stroke, a			
	Db	898 TGATCTGTTGAGCTGTTCCACTTGATGTCAGCAAGCTCAAGATGGAGTTG	957	CC	vascular irregularities or metabolic irregularities, associated with a			
	Qy	431 TTACACCCCTCAACTGGCTACTCCCTGCCTGTTG 467		CC	less active or non-active parkin protein			
	Db	958 TCCACGATGCTCACTTGCTACTCCCTGCGGTGT 994		XX	Sequence 3092 BP; 818 A; 778 C; 761 G; 735 T; 0 U; 0 Other;			
RESULT	8	Query Match	72.2%;	Score	340.2;	DB	4;	SQ
AAF55257	ID	AAF55257 standard; cDNA; 3092 BP.	Best Local Similarity	84.0%;	Pred.	No.	7e-107;	DR
XX	AC	AAF55257;	Matches	384;	Conservative	0;	Mismatches	p-PSDB;
XX	DT	29-MAY-2001 (first entry)	Indels	73;	Gaps	0;	Db	AB67550.
DE	DE	Nucleotide sequence of murine parkin2 with a frameshift mutation.	Qy	11	CAGGTAGATCACTACACAGCTTTCATCACTGCAAGGCTCAGTGGAGTTG	70	PT	
DE	DE	Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease;	Db	375 CAGTAAACCACTACACAGCTTTCATCACTGCAAGGCTCAGTGGAGTTG	434	PT		
KW	KW	Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis;	Qy	71 AGCGGGAAACTCGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGTC	130	PT		
KW	KW	Multi-system atrophy; Wilson's disease; Pick's disease; Prion disease;	Db	495 AGGGCCACRTTGTGCGAGGAGTCTTAATCCAAACGGATGAGTGTGAGT	554	PT		
KW	KW	brain tumour; head trauma; stroke; vascular irregularity;	Qy	191 CCCCAACTGCGTGGACTAGTGCAGAATTTCCTTAATGCGAGCACCCACCT	250	PT		
KW	KW	metabolic irregularity; ss.	Db	555 CTCCAGACTCCCTGGAACGAGCTGAGCTCAAGACCTCCAAACAGAACCT	494	PT		
OS	OS	Mus sp.	Db	615 CAGCAAGACAGCTCGTAGCTGTGAACTGATCACCGAACGACATCCCT	614	PT		
XX	PN	Location/Qualifiers	Qy	311 GCATTACGTGCAAGAGCTGAGGAGCCGCTGGTTTCCAGTGCACCTCCGCCAG	370	PT		
XX	FT	/tag= a	Db	675 GCATAGCGTGCAAGATGCTCAGGAGCCGCTGCTGTTCCGGTACACCGTCAG	734	PT		
XX	FT	/product= "truncated parkin2"	Qy	371 TGATTGCTGACTGCTGTTCCACTTAACTGTTGACAGACTCAATGATCGCAGTTG	430	PT		
XX	PN	EP1081225-A1.	Db	735 TGATCTGTTGGACTGTTCACTGTGATGTCAGAGACTCAACGATCGCGAGTTG	794	PT		
XX	PD	07-MAR-2001.	Qy	431 TTACACCCCTCAACTGGCTACTCCCTGCCTGTTG 467		PT		
XX	PR	30-AUG-1999;	Db	795 TCCACGAGCTCACTTGCTCCTCCCTGCGGTGT 831		PT		
XX	PA	(BIOF-) BIOFRONTERA PHARM GMBH.	Qy			PT		
PI	Luebbert H;		RESULT	9				
			AAF55256	ID	AAF55256 standard; cDNA; 3253 BP.			
			AC	AAF55256;				
			XX	DT	29-MAY-2001 (first entry)			
			XX	DE	Nucleotide sequence of murine parkin2 with a frameshift mutation.			

KW Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease;
 KW Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis;
 KW multi-system atrophy; Wilson's disease; Pick's disease; Prion disease;
 KW brain tumour; head trauma; stroke; vascular irregularity;
 KW metabolic irregularity; ss.
 OS Mus sp.
 XX Key location/Qualifiers
 PT CDS 129..362 /*tag= a /product= "truncated parkin2"
 PT PN EP1081225-A1.
 XX PD 07-MAR-2001.
 XX PR 30-AUG-1999; 99EP-00116766.
 XX PA (BIOF-) BIOFRONTERA PHARM GMBH.
 XX PI Luebbert H;
 XX DR WPI; 2001-212797/22.
 XX P-PSDB; AAB67529.
 XX PT New polynucleotides encoding mouse parkin2 protein, useful for producing
 PT a transgenic non-human animal as an animal model for neurodegenerative
 PT diseases.
 XX PS Claim 3; Page 33-34; 62pp; English.
 CC The present sequence encodes a murine parkin2 polypeptide. The
 CC polynucleotide sequence contains mutations causing Arg78 to be changed
 CC to a stop codon, leading to a truncated protein. Mutations or deletions
 CC in the parkin2 gene cause Parkinson's disease in humans. The human
 CC parkin2 gene is located in gene region 6q25.2-27. Parkin2 polypeptides
 CC and polynucleotides are useful for analysing neurodegenerative diseases.
 CC They are also useful for testing the efficacy of the treatment of a
 CC neurodegenerative disease such as Parkinson's disease, Alzheimer's
 CC disease, Huntington's disease, amyotrophic lateral sclerosis, Multi-
 CC system atrophy, Wilson's disease, Pick's disease, Prion disease, and
 CC secondary causes inducing Parkinson's syndromes like toxins, drugs, brain
 CC tumours, head trauma, stroke, vascular irregularities or metabolic
 CC irregularities, associated with a less active or non-active parkin
 XX protein
 XX Sequence 3253 BP; 851 A; 818 C; 808 G; 776 T; 0 U; 0 Other;
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 Best Local Similarity 84.0%; Pred. No. 7.2e-107;
 Matches 384; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
 Oy 11 CAGGTAGATCATCTACAACAGCTTATGTTGAAAGGCCCTTCAAAGATCC 70
 Db 536 CAGTTAACCCACCTACAACAGCTTTCATCTACTGCAGGGCCCTGCCAGGTCC 595
 Oy 71 AGCGGGAAAATCAGGGTACAGTGCAAGCTCCAGCTTCAACCTGACCC 130
 Db 596 AGCCCTGAGAACGCTCGAGTAGTGCTGGACCTGCAACAGCCTCCACCTTGCCCC 655
 Oy 131 AGGGTCCATCTGCTGGATGATTAACTCCAAACCGATGAGTGGTAATGCCAT 190
 Db 656 AGGSCCACTCTGCTGGAGGATGCTTAACTCCAAACCGATGAGTGGTAATGCCAT 715
 Oy 191 CCCACACACTGCCCCTGGAGTAGTGCAAGATTTCCTAAATGAGCACCCACCT 250
 Db 716 CTCCAGACTGCCCCTGGAGCACAGGTGAATTTCCTAAATGAGCACCCACCT 775
 Oy 251 CTGAAAGAACATCAGTAGTTGACCTGCGAACAAATGTCGACACTCACTT 310

Db 776 CAGACAAGAACACCTCGCTAGCTTGACCTGATCACCGAACAGGGCAGATCCCTT 815
 QY 311 GCATTAACCTGACAGACCTGAGAGCCGCTCCCTGTTCCAGTGCACTCCGCCCG 370
 Db 836 GCATAGCTGCAAGATGCTAGGAGCCCTGCTCTGCTCTCCAGTGTAACACCGTCACG 895
 QY 371 TGATTGCTTAGACTGTGTTCACTTATCTGTGACAGACTCAAT3ATCGGAGTTG 430
 Db 895 TGATCTGTTGACTGTGTTCACTGTGTAATGTPCAACATCGGCACTG 955
 QY 431 TTCAAGGACCTCAACTGCTACTCCCTGCTGCTGT 467
 Db 956 TCCACGAACTCAACTGCTACTCCCTGCTGCTGT 992

RESULT 10
 AAFF55254
 ID AAFF55254 standard; cDNA: 3253 BP.
 XX
 AC AAFF55254;
 XX DT 29-MAY-2001 (first entry)
 XX DE Nucleotide sequence of murine parkin2 with a frameshift mutation.
 XX Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease;
 KW Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis;
 KW multi-system atrophy; Wilson's disease; Pick's disease; Prion disease;
 KW brain tumour; head trauma; stroke; vascular irregularity;
 KW metabolic irregularity; ss.
 XX OS Mus sp.
 XX PI Luebbert H;
 XX PR 129..362 /*tag= a /product= "truncated parkin2"
 XX PT CDS PN EP1081225-A1.
 XX PD 07-MAR-2001.
 XX PR 30-AUG-1999; 99EP-00116766.
 XX PR 30-AUG-1999; 99EP-00116766.
 XX PA (BIOF-) BIOFRONTERA PHARM GMBH.
 XX PI Luebbert H;
 XX DR WPI; 2001-212797/22.
 XX P-PSDB; AAB67529.
 XX PT New polynucleotides encoding mouse parkin2 protein, useful for producing
 PT a transgenic non-human animal as an animal model for neurodegenerative
 PT diseases.
 XX PS Claim 3; Page 30-31; 62pp; English.
 CC The present sequence encodes a murine parkin2 polypeptide. The
 CC polynucleotide sequence contains mutations, causing Gln38 to be changed
 CC to a stop codon, leading to a truncated protein. Mutations or deletions
 CC in the parkin2 gene cause Parkinson's disease in humans. The human
 CC parkin2 gene is located in gene region 6q25.2-27. Parkin2 polypeptides
 CC and polynucleotides are useful for analysing neurodegenerative diseases.
 CC They are also useful for testing the efficacy of the treatment of a
 CC neurodegenerative disease such as Parkinson's disease, Alzheimer's
 CC disease, Huntington's disease, amyotrophic lateral sclerosis, Multi-
 CC system atrophy, Wilson's disease, Pick's disease, Prion disease, and
 CC secondary causes inducing Parkinson's syndromes like toxins, drugs, brain
 CC tumours, head trauma, stroke, vascular irregularities or metabolic
 CC irregularities, associated with a less active or non-active parkin
 CC protein

SQ	Sequence 3253	BP; 851 A; 818 C; 808 G; 776 T; 0 U; 0 Other;	PI	Luebert H;
Query Match	72.2%; Score 340.2; DB 4; Length 3253;	DR	WPI; 2001-212797/22.	
Best Local Similarity	84.0%; Pred. No. 7.2e-107;	DR	P-PSDB; AAB67528.	
Matches	384; Conservative 0; Mismatches 73; Indels 0; Gaps 0;	XX		
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Db	536 CAGTTAACCCACTACACAGCTTTCATCTACTGCAAGGCCCTCCACAGGTCC 595	PT		
OY	71 AGCGGGAAACTAGGGTACAGTCAGCACCTGAGGCAAGCAGCTTACCTGGCC 130	XX		
Db	596 AGCTTGGAAACTGGGAGTCAGTGTGGACCTGAAACAGCAAGCAGCTTACCTGGCC 555	PS	Claim 3; Page 31-32; 62pp; English.	
OY	131 AGGGTCACTTCTGGATGATCTTATTCAAACGGATGAGTGTGAATGCCAT 190	CC	The present sequence encodes a murine parkin polypeptide. The polynucleotide sequence contains mutations, causing Asn54 to be changed to a stop codon, leading to a truncated protein. Mutations or deletions in the parkin gene cause Parkinson's disease in humans. The human parkin gene is located in gene region 6q25.2-27. Parkin polypeptides and polynucleotides are useful for analyzing neurodegenerative diseases.	
Db	656 AGGCCCACTCTGGAGATCTTATTCAAACGGATGAGTGTGAATGCCAT 715	CC	They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, Multi-system atrophy, Wilson's disease, Pick's disease, Prion disease, and secondary causes inducing Parkinson's syndromes like toxins, drugs, brain tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated with a less active or non-active parkin protein.	
OY	191 CCCACACTGGCTGGGATAGTGGAGAATTTCTTAATGGAGACACCCACT 250	CC		
Db	716 CTCCAGACTGCCTGGACAGAGCTGAACTGGTAAATGGAGACACCCACT 775	CC		
OY	251 CTGACAAAGAACATCTAGCTGTTGACCTGTGCAACAAATGTCGAACTACTT 310	CC		
Db	776 CAGACAAAGAACATCTGGTAGCTTGAACCTGATAACCGAACAGGCGACATCCCT 835	CC		
OY	311 GCATTACTGACAGACGTCAGGGCCCGTCTGGTTCCAGTCACCTGGCCAG 370	XX		
Db	836 GCATAGCGCTGACAGATGTCAGGAGCCCTGCTCCAGTGTACCCAG 895	XX		
OY	371 TGAATGCTGAGTGTGTTACATATCTGTGACAGACTCATGATGGAGTGTG 430	CC		
Db	896 TGAATCTGTTGACTGTTACATGTATGTCACAGACTCACGATCGCCAGTTG 955	CC		
OY	431 TTGACGACCTCAACTTGCTACTCCCTGGCTGTGT 467	CC		
Db	956 TCCACGATGCTCAACTGGTACTCCTGGTGTGT 992	CC		
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ID		Query Match	72.2%; Score 340.2; DB 4; Length 3254;	
XX		Best Local Similarity	84.0%; Pred. No. 7.2e-107;	
AC		Matches	384; Conservative 0; Mismatches 73; Indels 0; Gaps 0;	
XX		OY	11 CAGGTAGATCACTACACAGCTTATGTTGATGTCAGGCAAGAGTGC 70	
DT		Db	537 CAGTTAACCCACCTACACAGCTTTCATCTACTGCAAGGCCCTGCCAGTCC 596	
29-MAY-2001 (first entry)		OY	71 AGCGGGAAACTGGTACAGTCAGGACACTCAGGGAGGCAAGCTTACCTGGACC 130	
XX		Db	597 AGCTTGAAGACTGGTAGTGTGCACTCTGCAACACCTTCACCTTGCCCC 656	
DE	Nucleotide sequence of murine parkin2 with a frameshift mutation.	XX		
XX	Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease; Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis; multi-system atrophy; Wilson's disease; Pick's disease; prion disease; brain tumour; head trauma; stroke; vascular irregularity; metabolic irregularity; ss.	XX		
OS	Mus sp.	XX		
XX	Key	Location/Qualifiers		
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PT	/product= "truncated parkin2"			
PN	EP1081225-A1.			
XX				
PD	07-MAR-2001.			
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PP	30-AUG-1999; 99EP-00116766.			
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PR	30-AUG-1999; 99EP-00116766.			
XX				
PA	(BIOF-) BIOPRONTERA PHARM GMBH.			
XX				
RESULT 12				
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XX		Best Local Similarity	84.0%; Pred. No. 7.2e-107;	
AC		Matches	384; Conservative 0; Mismatches 73; Indels 0; Gaps 0;	
XX		OY	371 TGAATGCTGAGTGTGTTACATGTATGTCACAGACTCACGATCGCCAGT 430	
FT		Db	897 TGAATCTGTTGACTGTTACATGTATGTCACAGACTCACGATCGCCAGT 956	
PT		OY	431 TTGACGACCTCAACTGGTACACTCCCTGGCTGTGT 467	
PN		Db	957 TCCACGATGCTCAACTGGTACTCCCTGGCTGTGT 993	
XX				

DE Nucleotide sequence of a mutated murine parkin2 polypeptide.
 XX
 KW Parkinson2; Parkinson's disease; 6q25.2-27; neurodegenerative disease;
 KW Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis;
 KW Multi-system atrophy; Wilson's disease; Pick's disease; Prion disease;
 KW head trauma; stroke; vascular irregularity;
 KW metabolic irregularity; ss.
 OS Mus sp.
 XX
 FH Key location/Qualifiers
 CDS 129..1523
 FT /*tag= a
 FT /product= "truncated parkin2"
 XX
 PN EP1081225-A1.
 XX
 PD 07-MAR-2001.
 XX
 PF 99EP-00116766.
 XX
 PR 30-AUG-1999; 99EP-00116766.
 XX
 PA (BIOF-) BIOPRONTERA PHARM GMBH.
 XX
 PT Luebbert H;
 XX
 DR WPI; 2001-212797/22.
 DR P-PSDB; AAB67532.
 XX
 PT New poly nucleotides encoding mouse parkin2 protein, useful for producing
 PT a transgenic non-human animal as an animal model for neurodegenerative
 PT diseases.
 XX
 PS Claim 3; Page 36-38; 62pp; English.
 XX
 CC The present sequence encodes a murine parkin2 polypeptide. The sequence
 CC contains the mutation Thr41Asn. Mutations or deletions in the parkin2
 gene cause Parkinson's disease in humans. The human parkin gene is
 CC located in gene region 6q25.2-27. Parkin2 polypeptides and
 CC poly nucleotides are useful for analysing neurodegenerative diseases. They
 CC are also useful for testing the efficacy of the treatment of a
 CC neurodegenerative disease such as Parkinson's disease, Alzheimer's
 CC disease, Huntington's disease, amyotrophic lateral sclerosis, Multi-
 CC system atrophy, Wilson's disease, Pick's disease, Prion disease, and
 CC secondary causes inducing Parkinson's syndromes like toxins, drugs, brain
 CC tumours, head trauma, stroke, vascular irregularities or metabolic
 CC irregularities, associated with a less active or non-active parkin
 CC protein.
 XX
 SQ Sequence 3255 BP; 853 A; 817 C; 809 G; 776 T; 0 U; 0 Other;
 Best Local Similarity 72.2%; Score 340.2; DB 4; Length 3255;
 Matches 384; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
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 Db 538 CAGTTAACCCACCTACAGCTTTCATCTACTGCAAAGGCCCTGCAAGGTCC
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 Query Match 71 AGCCGGAAACACTCGGGTACGGCAGCCGACCTTGACCC 130
 Qy 598 AGCCCTGGAAGCTCGAGTTCAGTGTGGACCTGCAACAGCACTTCACCTGGCC 657
 Qy 131 AGGGTCCATCTGTGGATGATGTTTAATCCAAACGGATGAGTGGATGCAAT 190
 Db 658 AGGGCCACATCTGCAGGAGATGCTTAATCCAAACGGATGAGTGGATGCACT 717
 Qy 191 CCCACACTGCCCCTGGACTATGTCAGATTCTTAAATGCGGACACCCACCT 250
 Db 718 CTCCAGACTGCCCTGGAACGAGCTGAATTTCCTTAAATGCGGAGCACCAACT 777
 XX
 251 CTGACAAGGAAACATCAGTAGCTTGCACCTGACAAATAGTCGGACATCACTT 310

RESULT 13
 AAF55244
 ID AAF55244 standard; cDNA; 3255 BP.
 XX
 AC AAF55244;
 XX
 DT 29-MAY-2001 (first entry)
 XX
 DE Nucleotide sequence of a murine parkin2 polypeptide.
 XX
 Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease;
 KW Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis;
 KW Multi-system atrophy; Wilson's disease; Pick's disease; Prion disease;
 KW head trauma; stroke; vascular irregularity;
 KW metabolic irregularity; ss.
 XX
 OS Mus sp.
 XX
 FH Key location/Qualifiers
 CDS 129..1523
 FT /*tag= a
 FT /product= "parkin2"
 XX
 PN EP1081225-A1.
 XX
 PD 07-MAR-2001.
 XX
 PF 30-AUG-1999; 99EP-00116766.
 XX
 PR 30-AUG-1999; 99EP-00116766.
 XX
 PA (BIOF-) BIOPRONTERA PHARM GMBH.
 XX
 PT Luebbert H;
 XX
 DR WPI; 2001-212797/22.
 DR P-PSDB; AAB67517.
 XX
 PT New poly nucleotides encoding mouse parkin2 protein, useful for producing
 PT a transgenic non-human animal as an animal model for neurodegenerative
 PT diseases.
 XX
 Disclosure; Page 15-16; 62pp; English.
 XX
 The present sequence encodes a murine parkin2 polypeptide. Mutations or
 CC deletions in the parkin2 gene cause Parkinson's disease in humans. The
 human parkin gene is located in gene region 6q25.2-27. Parkin2
 CC polypeptides and poly nucleotides are useful for analysing
 CC neurodegenerative diseases. They are also useful for testing the efficacy
 CC of the treatment of a neurodegenerative disease such as Parkinson's
 CC disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral
 CC sclerosis, Multi-system atrophy, Wilson's disease, Pick's disease, Prion
 CC disease, and secondary causes inducing Parkinson's syndromes like toxins,
 CC drugs, brain tumours, head trauma, stroke, vascular irregularities or
 CC metabolic irregularities, associated with a less active or non-active
 CC parkin protein.

Db 778 CAGACAAGACACCTCGTAGCTTGACCTGATCACGCAACAGGCCAGATCCCT 837
 QY 311 GCATTACCTGCACAGACCTCAGGAGCCGCTCGGTTCCAGTCACTCGCCCG 370
 Db 838 GCATAGCTGCACAGATTCAGTCAGCCCTGCTTGCTTGCTTGCTTG 897
 QY 371 TGATTGCTTAGCTGTTCACITATCTGTGACAGACTCATGATCGGAGTTG 430
 Db 898 TGATCTGTTGGACTGTTCACITGTATGTGTCACAGACTCAACGATCGGAGTTG 957
 QY 431 TTCCAGAACCTCAACTTGCTACTCCCTCCCTGTT 467
 Db 958 TCCACGATGCTCAACTTGCTACTCCCTCCCTGTT 994

SQ	Sequence	3255	BP;	852	A;	818	C;	809	G;	776	T;	0	U;	0	Other;
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Best Local Similarity	84.0%	Pred.	No.	7.2e-107;											
Matches	384;	Conservative		0;	Mismatches	73;	Indels	0;	Gaps	0;					
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PT	DR	P-PSDB; AAB7533.													
PT	XX	The present sequence encodes a murine parkin2 polypeptide. The sequence contains the mutation Trp53Stop. Mutations or deletions in the parkin2 gene cause Parkinson's disease in humans. The human parkin2 gene is located in gene region 6q25.2-21. Parkin2 polydepletions and polymucleotides are useful for analysing neurodegenerative diseases. They are also useful for testing the efficacy of the treatment of a neurodegenerative disease such as Parkinson's disease, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, Multi-system atrophy, Wilson's disease, Pick's disease, Prion disease, and secondary causes inducing Parkinson's syndrome like toxins, drugs, brain tumours, head trauma, stroke, vascular irregularities or metabolic irregularities, associated with a less active or non-active Parkin protein.													
PT	XX	Claim 3; Page 38-39; 62pp; English.													
PS	XX	Sequence 3255 BP; 852 A; 818 C; 808 G; 776 T; 0 U; 0 Other;													
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Best Local Similarity	84.0%	Pred.	No.	7.2e-107;											
Matches	384;	Conservative		0;	Mismatches	73;	Indels	0;	Gaps	0;					
PT	CC	11 CAGGTAGATCAACTACAGAACGTTTAATGCTTATGGTCAAGGCCCTGTCAGAACAGTCAC 370													
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PT	CC	371 TGATTGCTTAGCTGTTCACTTACTGTGAGAACACTCATGATCGGAGTTG 430													
PT	CC	Db 898 TGATCCTGTTGACTGTTCACCTGATGGTCAAGACTCAACGATCGGAGTTG 957													
PT	CC	QY 431 TTGACGACCTCTAACCTGGCTACTCCCTGCGCTGT 467													
PT	CC	Db 958 TCCACGATGCTAACCTGGCTACTCCCTGCGCTGT 994													
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PT	XX	AAF55260													
PT	XX	ID AAF55260 standard; cDNA; 3255 BP.													
PT	XX	AAF55260;													
PT	XX	AC													
PT	XX	DT 29-MAY-2001 (first entry)													
PT	XX	DE Nucleotide sequence of a mutated murine parkin2 polypeptide.													
PT	XX	XX Parkinson2; Parkinson's disease; 6q25.2-27; neurodegenerative disease; Lewy bodies; Huntington's disease; amyotrophic lateral sclerosis; Multi-system atrophy; Wilson's disease; Pick's disease; Prion disease; brain tumour; head trauma; stroke; vascular irregularity; metabolic irregularity; ss.													
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PT	XX	AC AAF55258;													
PT	XX	DT 29-MAY-2001 (first entry)													
PT	XX	DE Nucleotide sequence of a mutated murine parkin2 polypeptide.													
PT	XX	Luebbert H;													

KW Parkin2; Parkinson's disease; 6q25.2-27; neurodegenerative disease;
 KW Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis;
 KW multi-system atrophy; Wilson's disease; Pick's disease; Prion disease;
 KW brain tumour; head trauma; stroke; vascular irregularity;
 KW metabolic irregularity; ss.

XX OS Mus sp.

XX PH Key location/Qualifiers

XX PT CDS /*tag= a

PT /product= "truncated parkin2"

XX PN BP1081225-A1.

XX PD 07-MAR-2001.

XX PR 30-AUG-1999; 99EP-00116765.

XX PR 30-AUG-1999; 99EP-00116766.

XX PA (BIOF-) BIOFRONTERA PHARM GMBH.

XX PI Juebbert H;

XX DR WPI; 2001-212797/22.

DR P-PSDB; AAB67531.

XX PT New polynucleotide encoding mouse parkin2 protein, useful for producing
 PT a transgenic non-human animal as an animal model for neurodegenerative
 PT diseases.

XX PS Claim 3; Page 35-36; 62pp; English.

CC The present sequence encodes a murine parkin2 polypeptide. The sequence
 CC contains the mutation Lys161Asn. Mutations or deletions in the parkin2
 CC gene cause Parkinson's disease in humans. The human parkin2 gene is
 CC located in gene region 6q25.2-27. Parkin2 polypeptides and
 CC polynucleotides are useful for analysing neurodegenerative diseases. They
 CC are also useful for testing the efficacy of the treatment of a
 CC neurodegenerative disease such as Parkinson's disease, Alzheimer's
 CC disease, Huntington's disease, amyotrophic lateral sclerosis, Multi-
 CC system atrophy, Wilson's disease, Pick's disease, Prion disease, and
 CC secondary causes inducing Parkinson's syndromes like toxins, drugs, brain
 CC tumours, head trauma, stroke, vascular irregularities or metabolic
 CC irregularities, associated with a less active or non-active parkin
 CC protein

XX SQ Sequence 3255 BP; 852 A; 818 C; 808 G; 777 T; 0 U; 0 Other;

Query Match 72.2%; Score 340.2; DB 4;
 Best Local Similarity 84.0%; Pred. No. 7.2e-107;
 Matches 384; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

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  QY 11 CAGCTAGATCATCTACAAACGCTTATGTTGTTATGCCAAAGGCCCTCTCAAGAGTC 70
  DB 538 CAGTAAACCCACTACACAGCTTTTCATCTACTGCAGAACGCCCCCTGCCACAGGCC 597
  QY 71 AGCGGGAAACATCAGGGTACAGTGCGACCTCGAGGAGGCAACGGCTCACCTGACCC 130
  DB 598 AGCTTGGAATCTCGAGATCAGTGCGACCTCGCAACAGAACCTTCAACCTGGCC 657
  QY 131 AGGGTCCATCTCTGGATGATGTTTATCCAAACGGGAGGTGATGCGCAAT 190
  DB 718 CTCCAGACTGCCCTGGAACAGCAAGCTGTAATTTCCTTAATGAGCACCCAACT 777
  QY 251 CTGACAAGAACATCAGTAGCTTGACCTGATGCAACAAATAGTCGAAACATCACTT 310
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SUMMARIES

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5	251.8	53.5	2513	4 US-09-649-016-983	Sequence 983, AppI
6	37.8	8.0	399	4 US-09-621-976-8976	Sequence 976, AppI
7	34.8	7.4	40	4 US-09-601-844B-65	Sequence 65, AppI
8	34.8	7.4	361	3 US-09-643-597-293	Sequence 293, AppI
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18	32.6	6.9	35263	4 US-09-949-016-16399	Sequence 16399, A
19	32.2	6.8	152132	4 US-09-949-016-13845	Sequence 13845, A
20	32.2	6.8	152145	4 US-09-949-016-12371	Sequence 12371, A
21	32	6.8	38	4 US-09-601-844B-66	Sequence 66, AppI
22	32	6.8	347	4 US-09-621-976-11665	Sequence 11665, A
23	32	6.8	819	4 US-09-489-039A-3239	Sequence 3239, AppI
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ALIGNMENTS

RESULT 1

US-09-601-844B-1

Sequence 1, Application US/09601844B
; Patent No. 6716621

GENERAL INFORMATION:

; APPLICANT: Shimizu, No. 6716621uyoshi

; TITLE OF INVENTION: Isolated DNA or Gene Responsible for Parkinson's Disease

; FILE REFERENCE: 0652_2110000

; CURRENT APPLICATION NUMBER: US/09/601,844B

; CURRENT FILING DATE: 2000-08-09

; PRIOR APPLICATION NUMBER: PCT/JP99/00545

; PRIOR FILING DATE: 1999-02-09

; NUMBER OF SEQ ID NOS: 70

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO: 1

; LENGTH: 2960

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE: misc feature

; NAME/KEY: CDS

; LOCATION: (102)..(1496)

; OTHER INFORMATION:

; FEATURE: misc feature

; NAME/KEY: misc feature

; LOCATION: (102)..(108)

; OTHER INFORMATION: exon 1

; FEATURE: misc feature

; NAME/KEY: misc feature

; LOCATION: (109)..(272)

; OTHER INFORMATION: exon 2

; FEATURE: misc feature

; NAME/KEY: misc feature

; LOCATION: (273)..(513)

; OTHER INFORMATION: exon 3

; FEATURE: misc feature

; NAME/KEY: misc feature

; LOCATION: (514)..(635)

; OTHER INFORMATION: exon 4

; FEATURE: misc feature

; NAME/KEY: misc feature

; LOCATION: (636)..(719)

; OTHER INFORMATION: exon 5

; FEATURE: misc feature

; NAME/KEY: misc feature

; LOCATION: (836)..(972)

OTHER INFORMATION: Exon 7
; FEATURE: misc feature
; LOCATION: (973)..(1034)
; OTHER INFORMATION: Exon 8
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1035)..(1184)
; OTHER INFORMATION: Exon 9
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1185)..(1268)
; OTHER INFORMATION: Exon 10
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1269)..(1386)
; OTHER INFORMATION: Exon 11
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1387)..(2960)
; OTHER INFORMATION: Exon 12
; US-09-601-844B-1

Query Match 99.0%; Score 466.4; DB 4; Length 2960;
Best Local Similarity 99.8%; Pred. No. 1.9e-154; Matches 467; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAAGTCAGGAGGTAGATCATTCAACAGCTTATGNGTATGCAAGGCCCTGT 60
Db 504 GGAAGTCAGGAGGTAGATCATTCAACAGCTTATGNGTATGCAAGGCCCTGT 563
Qy 61 CAAAGAGTGCGCCGGAAACTCAGGTTAGTGCGACCTGCAGGCCAGCTC 120
Db 564 GGAAGTCAGGAGGTAGATCATTCAACAGCTTATGNGTATGNGTATGCAAGGCCCTGT 563
Qy 121 ACCTGACCCAGGGTCATCTGCTGGATAATGTTAATCCAAACCGATAGTGT 180
Db 624 ACCTGACCCAGGGTCATCTGCTGGATAATGTTAATCCAAACCGATAGTGT 683
Qy 181 GAAATGCCATCCCAACTGCGCTGGACTAGTGCGAAGAATTCTTAAATGGGACA 240
Db 684 GAAATGCCATCCCAACTGCGCTGGACTAGTGCGAAGAATTCTTAAATGGGACA 743
Qy 301 AACATCCTGATTACCGCACAGCTCAGGAGCCGCTGGTTTCAGTCAC 360
Db 744 AACATCCTGATTACCGCACAGCTCAGGAGCCGCTGGTTTCAGTCAC 803
Qy 301 AACATCCTGATTACCGCACAGCTCAGGAGCCGCTGGTTTCAGTCAC 360
Db 804 AACATCCTGATTACCGCACAGCTCAGGAGCCGCTGGTTTCAGTCAC 863
Qy 361 TCCGGCCCGTGTGATTGGCTAGCTTCACTTAATCTGTGACAGACTCATGAT 420
Db 864 TCCGGCCCGTGTGATTGGCTAGCTTCACTTAATCTGTGACAGACTCATGAT 923
Qy 421 CGCGAGTTGTCAAGGACCTCAACTTGCTRACTCTGCCTGGTG 468
Db 924 CGCGAGTTGTCAAGGACCTCAACTTGCTRACTCTGCCTGGTG 971

RESULT 2
US-09-949-016-645
; Sequence 645, Application US/09949016
; Patent No. 6,812,339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR FILING DATE: 2000-10-20

Query Match 99.0%; Score 466.4; DB 4; Length 2960;
Best Local Similarity 99.8%; Pred. No. 1.9e-154; Matches 467; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAAGTCAGGAGGTAGATCATTCAACAGCTTATGNGTATGCAAGGCCCTGT 60
Db 504 GGAAGTCAGGAGGTAGATCATTCAACAGCTTATGNGTATGCAAGGCCCTGT 563
Qy 61 CAAAGAGTGCGCCGGAAACTCAGGTTAGTGCGACCTGCAGGCCAGCTC 120
Db 564 GGAAGTCAGGAGGTAGATCATTCAACAGCTTATGNGTATGCAAGGCCCTGT 563
Qy 121 ACCTGACCCAGGGTCATCTGCTGGATAATGTTAATCCAAACCGATAGTGT 180
Db 624 ACCTGACCCAGGGTCATCTGCTGGATAATGTTAATCCAAACCGATAGTGT 683
Qy 181 GAAATGCCATCCCAACTGCGCTGGACTAGTGCGAAGAATTCTTAAATGGGACA 240
Db 684 GAAATGCCATCCCAACTGCGCTGGACTAGTGCGAAGAATTCTTAAATGGGACA 743
Qy 241 CACCCCACTCTGACAGGAAACATCAGGTTACCTGCACATGCAACAACTGCG 300
Db 744 CACCCCACTCTGACAGGAAACACAGCTAGCTTGACCTGCACATGCAACAACTGCG 803
Qy 301 AACATCCTGATTACCGCACAGCTCAGGAGCCGCTGGTTTCAGTCAC 360
Db 804 AACATCCTGATTACCGCACAGCTCAGGAGCCGCTGGTTTCAGTCAC 863
Qy 361 TCCGGCCCGTGTGATTGGCTAGCTTCACTTAATCTGTGACAGACTCATGAT 420
Db 864 TCCGGCCCGTGTGATTGGCTAGCTTCACTTAATCTGTGACAGACTCATGAT 923
Qy 421 CGCGAGTTGTCAAGGACCTCAACTTGCTRACTCTGCCTGGTG 468
Db 924 CGCGAGTTGTCAAGGACCTCAACTTGCTRACTCTGCCTGGTG 971

RESULT 3
US-09-601-844B-3
; Sequence 3, Application US/09601844B
; Patent No. 6,716,621
; GENERAL INFORMATION:
; APPLICANT: Shimizu, Mizuno, Yoshihiko
; TITLE OF INVENTION: Isolated DNA or Gene Responsible for Parkinson's Disease
; FILE REFERENCE: 0652-2110000
; CURRENT APPLICATION NUMBER: US/09/601, 844B
; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: PCT/JP99/00545
; PRIOR FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2876
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1021)..(1412)
; OTHER INFORMATION:

FEATURE:

NAME/KEY: misc feature
 LOCATION: (102)..
 OTHER INFORMATION: Exon 1
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (109)..
 OTHER INFORMATION: Exon 2
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (154)..
 OTHER INFORMATION: Exon 3
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1889)..
 OTHER INFORMATION: Exon 4
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (752)..
 OTHER INFORMATION: Exon 6
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (951)..
 OTHER INFORMATION: Exon 7
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (110)..
 OTHER INFORMATION: Exon 9
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1184)
 OTHER INFORMATION: Exon 10
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1185)..
 OTHER INFORMATION: Exon 11
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1303)..
 OTHER INFORMATION: Exon 11
 US-09-601-844B-3

Query Match 61.2%; Score 288.4; DB 4; Length 2876;
 Best Local Similarity 81.8%; Pred. No. 2.7e-91; Mismatches 1; Indels 84; Gaps 1;
 Matches 383; Conservative 0; Mismatches 1; Indels 84; Gaps 1;

QY 1 GGAAGTCCAGGGATGATCACTACAACAGCTTTATGTGATTGCAAGGCCCTGT 60
 Db 504 GGAAGTCAGCAGGGTAGATCATCTACAGCTTACAGCTTATGTGATTGCAAGGCCCTGT 563
 QY 61 CAAAGAGTGCAGCGGAAACTCAGGGTACAGTGCAAGCTGCA3GCGCAACGCTC 120
 Db 564 CAAAGAGTGCAGCGGAAACTCAGGGTACAGTGCAAGCTGCA3GCGCAACGCTC 623
 QY 121 ACCTGACCCAGGGTCATCTGCTGGATGATGTTTATTCAAACGGATGAGTGGT 180
 Db 624 ACCTGACCCAG-----635
 Db 181 GAATGCCAATCCCCAACACTGCCCTGGACTAGTGCAAGATTCTTAATGGAGCA 240
 QY 636 -----GANTTTCTTAATGGAGCA 659
 QY 121 ACCTGACCCAGGGTCATCTGCTGGATGATGTTTATTCAAACGGATGAGTGGT 180
 Db 624 ACCTGACCCAG-----635
 Db 720 AACATCACTGCAATTGCACTGGCACAGCTGCAAGCCGCTGGTTCCAGTGCAAC 779
 QY 181 GAATGCCAATCCCCAACACTGCCCTGGACTAGTGCAAGATTCTTAATGGAGCA 240
 Db 660 CACCCCACTCTGCAAAAGAACACAGTAGCTTGCACTGTGCAACAAATAGTCGG 659
 QY 241 CACCCACCTCTGCAAAAGAACACAGTAGCTTGCACTGTGCAACAAATAGTCGG 300
 Db 660 CACCCCACTCTGCAAAAGAACACAGTAGCTTGCACTGTGCAACAAATAGTCGG 719
 QY 301 AACATCACTGCAATTGCACTGGCACAGCTGCAAGCCGCTGGTTCCAGTGCAAC 360
 Db 780 TCCGCCACCTGATTTGCTAGCTTACCTGACAGACTCATGATGCAACAAATAGTCGG 839
 QY 421 CGGCACTGTTCTGCAAGCCCTCAACTTGCCTCTGTTCCAGTGCAAC 468
 Db 840 CGGCAGTTCTCACGACCTCAACTTGCTGACTCCCTGCTGGTG 887

RESULT 4
 US-09-949-016-982
 ; Sequence 982 Application US/09949016
 ; GENERAL INFORMATION:
 ; PATENT NO. 6812339
 ; APPLICANT: VENSTER, J. Craig et al.
 ; TITLE OR INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949, 016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241, 755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237, 768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231, 498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 20712
 ; SOFTWARE: PastSeq for Windows Version 4.0
 ; SEQ ID NO: 982
 ; LENGTH: 2876
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-982

Query Match 61.2%; Score 288.4; DB 4; Length 2876;
 Best Local Similarity 81.8%; Pred. No. 2.7e-91; Mismatches 1; Indels 84; Gaps 1;
 Matches 383; Conservative 0; Mismatches 1; Indels 84; Gaps 1;

QY 1 GGAAGTCCAGGGTAGATCATCTACAGCTTATGTGATTGCAAGGCCCTGT 60
 Db 504 GGAAGTCAGCAGGGTAGATCATCTACAGCTTATGTGATTGCAAGGCCCTGT 563
 QY 61 CAAAGAGTGCAGCGGAAACTCAGGGTACAGTGCAAGCTGCA3GCGCAACGCTC 120
 Db 564 CAAAGAGTGCAGCGGAAACTCAGGGTACAGTGCAAGCTGCA3GCGCAACGCTC 623
 QY 121 ACCTGACCCAGGGTCATCTGCTGGATGATGTTTATTCAAACGGATGAGTGGT 180
 Db 624 ACCTGACCCAG-----635
 Db 181 GAATGCCAATCCCCAACACTGCCCTGGACTAGTGCAAGATTCTTAATGGAGCA 240
 QY 636 -----GANTTTCTTAATGGAGCA 659
 QY 241 CACCCACCTCTGCAAAAGAACACAGTAGCTTGCACTGTGCAACAAATAGTCGG 300
 Db 660 CACCCCACTCTGCAAAAGAACACAGTAGCTTGCACTGTGCAACAAATAGTCGG 719
 QY 301 AACATCACTGCAATTGCACTGGCACAGCTGCAAGCCGCTGGTTCCAGTGCAAC 360
 Db 780 TCCGCCACCTGATTTGCTAGCTTACCTGACAGACTCATGATGCAACAAATAGTCGG 839
 QY 421 CGGCACTGTTCTGCAAGCCCTCAACTTGCCTCTGTTCCAGTGCAAC 468
 Db 840 CGGCAGTTCTCACGACCTCAACTTGCTGACTCCCTGCTGGTG 887

RESULT 5
 US-09-949-016-983

```

; Sequence 983, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR FILING DATE: 2000-10-20
; PRIORITY NUMBER: 60/237, 768
; PRIORITY FILING DATE: 2000-10-03
; PRIORITY NUMBER: 60/231, 498
; PRIORITY FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 983
; LENGTH: 2513
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-983

Query Match
Best Local Similarity 53.5%; Score 251.8; DB 4; Length 2513;
Matches 256; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 206 GCACTAGTGCGAATTTCTTAATGTCGACACCCACCTCTGACAAGAACAT 265
Db 262 GCACTGTGACGAAATTTCCTTAATGTCGACACCCACCTCTGACAAGAAC 321
QY 266 CAGTAGCTTGACCTGTGACAAATAGTCGACACTCCTGCACTGCAAGCAC 325
Db 322 CAGTAGCTTGACCTGTGACAAATAGTCGACACCCACCTCTGACAAGAAC 381
QY 326 AGTCGGACCCGCTCTGGTTTCAGGCCACTCCCGCAGCTGATTCAGCT 385
Db 382 AGTGTGGACGCCGCTCTGGTTTCAGGCCACTCCGCCAGCTGATTCAGCT 441
QY 386 GTTCACTTAACTGTGCAAGACTCATGATGGCAGTTGTTCAAGACCTCAC 445
Db 442 GTTCACTTAACTGTGCAAGACTCATGATGGCAGTTGTTCAAGACCTCAC 501
QY 446 TGGCTACTCCCTGCCTTGTTG 468
Db 502 TGGCTACTCCCTGCCTTGTTG 524

RESULT 6
; Sequence 8976, Application US/09621976
; Patent No. 663903
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET-054-PR2
; CURRENT APPLICATION NUMBER: US/09/621, 976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO: 8976
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-621-976-8976

Query Match
Best Local Similarity 97.3%; Score 251.8; DB 4; Length 2513;
Matches 256; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 206 GCACTAGTGCGAATTTCTTAATGTCGACACCCACCTCTGACAAGAACAT 265
Db 262 GCACTGTGACGAAATTTCCTTAATGTCGACACCCACCTCTGACAAGAAC 321
QY 266 CAGTAGCTTGACCTGTGACAAATAGTCGACACTCCTGCACTGCAAGCAC 325
Db 322 CAGTAGCTTGACCTGTGACAAATAGTCGACACCCACCTCTGACAAGAAC 381
QY 326 AGTCGGACCCGCTCTGGTTTCAGGCCACTCCCGCAGCTGATTCAGCT 385
Db 382 AGTGTGGACGCCGCTCTGGTTTCAGGCCACTCCGCCAGCTGATTCAGCT 441
QY 386 GTTCACTTAACTGTGCAAGACTCATGATGGCAGTTGTTCAAGACCTCAC 445
Db 442 GTTCACTTAACTGTGCAAGACTCATGATGGCAGTTGTTCAAGACCTCAC 501
QY 446 TGGCTACTCCCTGCCTTGTTG 468
Db 502 TGGCTACTCCCTGCCTTGTTG 524

RESULT 7
; Sequence 601-844B-65
; Patent No. 6715621
; GENERAL INFORMATION:
; APPLICANT: Mizuno, Yoshiaki
; TITLE OF INVENTION: Isolated DNA or Gene Responsible for Parkinson's Disease
; FILE REFERENCE: 0522-121000
; CURRENT APPLICATION NUMBER: US/09/601, 844B
; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: PCT/JP99/00545
; PRIORITY NUMBER: PCT/JP99/00545
; PRIORITY FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 65
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-601-844B-65

Query Match
Best Local Similarity 94.7%; Score 34.8; DB 4; Length 40;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 128 CCCAGGTTCCATCTGGATGATGTTAATCCA 165
Db 3 CCAAAGGTCATCTGGATGATGTTAATCCA 40

RESULT 8
; Sequence 293, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangir, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeley, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; Query Match
; Best Local Similarity 8.0%; Score 37.8; DB 4; Length 399;
; Matches 36; Conservative 134; Mismatches 131; Indels 0; Gaps 0;
; US-09-621-976-8976
; Query Match
; Best Local Similarity 12.0%; Score 37.8; DB 4; Length 399;
; Matches 36; Conservative 134; Mismatches 131; Indels 0; Gaps 0;
; US-09-949-016-983

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CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 293
LENGTH: 361
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(361)
OTHER INFORMATION: n = A,T,C or G
US-09-643-597-293

Query Match 7.4%; Score 34.8; DB 3; Length 361;
Best Local Similarity 59.4%; Pred. No. 0.076; Mismatches 0; Indels 0; Gaps 0;
Matches 57; Conservative 0; MisMatches 39; Indels 0; Gaps 0;

QY 203 CTGGGACTAGTGCGAGATTTCCTTAATGTGGAGCACACCCACCTCTGACAGGAA 262
Db 134 CTTGACACGCTTCAATTCTTCCTTCCAATATGCTGCATGCCACACTTGAGGTAACGAAG 193

QY 263 CATCAGTAGCTTGACCTGATGCGACAAATAGTC 298
Db 194 CANAAGTATTTTAACATGACAGCTTANACATTC 229

RESULT 9
US-09-480-884A-293
Sequence 293, Application US/0940884A
; Patent No. 6482597
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fang, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 293
LENGTH: 361
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(361)
OTHER INFORMATION: n = A,T,C or G
US-09-480-884A-293

Query Match 7.4%; Score 34.8; DB 4; Length 361;
Best Local Similarity 59.4%; Pred. No. 0.076; Mismatches 39; Indels 0; Gaps 0;
Matches 57; Conservative 0; MisMatches 39; Indels 0; Gaps 0;

QY 203 CTGGGACTAGTGCGAGATTTCCTTAATGTGGAGCACACCCACCTCTGACAGGAA 262
Db 134 CTTGACACGCTTCAATTCTTCCTTCCAATATGCTGCATGCCACACTTGAGGTAACGAAG 193

QY 263 CATCAGTAGCTTGACCTGATGCGACAAATAGTC 298
Db 194 CANAAGTATTTTAACATGACAGCTTANACATTC 229

RESULT 11
US-09-606 421B-293
Sequence 293, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Fang, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Ajun
; APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 293
LENGTH: 361
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(361)
OTHER INFORMATION: n = A,T,C or G
US-09-606-421B-293

Query Match 7.4%; Score 34.8; DB 4; Length 361;
Best Local Similarity 59.4%; Pred. No. 0.076; Mismatches 0; Indels 0; Gaps 0;
Matches 57; Conservative 0; MisMatches 39; Indels 0; Gaps 0;

QY 203 CTGGGACTAGTGCGAGATTTCCTTAATGTGGAGCACACCCACCTCTGACAGGAA 262
Db 134 CTTGACACGCTTCAATTCTTCCTTCCAATATGCTGCATGCCACACTTGAGGTAACGAAG 193

QY 263 CATCAGTAGCTTGACCTGATGCGACAAATAGTC 298
Db 194 CANAAGTATTTTAACATGACAGCTTANACATTC 229

RESULT 10
US-09-542-615A-293
Sequence 293, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fang, Gary R.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Fang, Gary R.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fan, Liqun
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Ajun
; APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 293
LENGTH: 361
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(361)
OTHER INFORMATION: n = A,T,C or G
US-09-542-615A-293

Query Match 7.4%; Score 34.8; DB 4; Length 361;
Best Local Similarity 59.4%; Pred. No. 0.076; Mismatches 0; Indels 0; Gaps 0;
Matches 57; Conservative 0; MisMatches 39; Indels 0; Gaps 0;

QY 203 CTGGGACTAGTGCGAGATTTCCTTAATGTGGAGCACACCCACCTCTGACAGGAA 262
Db 134 CTTGACACGCTTCAATTCTTCCTTCCAATATGCTGCATGCCACACTTGAGGTAACGAAG 193

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RESULT 12 7.4%; Score 34.8; DB 4; Length 405;
 US-09-630-940B-293
 ; Sequence 293, Application US/09630940B
 ; Patent No. 6717514
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Fan, Liqun
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Hosken, Nancy
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: McNeill, Patricia D.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
 FILE REFERENCE: 210121-455C10
 CURRENT APPLICATION NUMBER: US/09/630,940B
 CURRENT FILING DATE: 2000-08-02
 NUMBER OF SEQ ID NOS: 367
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 293
 LENGTH: 361
 TYPE: DNA
 ORGANISM: Homo sapien
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(361)
 OTHER INFORMATION: n = A,T,C or G
 US-09-630-940B-293

Query Match 7.4%; Score 34.8; DB 4; Length 361;
 Best Local Similarity 59.4%; Pred. No. 0.076;
 Matches 57; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 203 CTGGGACTAGTGAGAAATTCTTAAATGGAGCACACCCACCTCTGACAAGGAA 262
 Db 134 CTTGAAACAGTCCTCAATTCTCTCAAAATGCTGCATGCGACATTGGTAGGAAG 193

QY 263 CATCAGTAGCTTGCACTGTGATGCGACAAATAGTC 298
 Db 194 CAAAGATTTAACATGACAGCTTAAACATTC 229

RESULT 13 7.4%; Score 34.8; DB 4; Length 405;
 US-09-513-999C-11324/c
 ; Sequence 11324, Application US/09513999C
 ; Patent No. 6783961
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Ducart, A.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
 ; Patent No. 6783961
 ; FILE REFERENCE: 59.US2. REG
 ; CURRENT APPLICATION NUMBER: US/09/513,999C
 ; CURRENT FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/122,487
 ; PRIOR FILING DATE: 1999-02-26
 ; NUMBER OF SEQ ID NOS: 36681
 ; SOFTWARE: Patent-PM
 ; SEQ ID NO 11324
 LENGTH: 405
 TYPE: DNA
 ORGANISM: Homo sapiens

RESULT 14 7.4%; Score 34.8; DB 4; Length 405;
 US-09-601-844B-64
 ; Sequence 64, Application US/09601844B
 ; Patent No. 6716621
 ; GENERAL INFORMATION:
 ; APPLICANT: Shimizu, No. 6716621uyoshi
 ; APPLICANT: Mizuno, Yoshihuni
 ; TITLE OF INVENTION: Isolated DNA or Gene Responsible for Parkinson's Disease
 FILE REFERENCE: 0652-211000
 CURRENT APPLICATION NUMBER: US/09/601,844B
 CURRENT FILING DATE: 2000-08-09
 PRIORITY APPLICATION NUMBER: PCT/JP99/00545
 PRIOR FILING DATE: 1999-02-09
 NUMBER OF SEQ ID NOS: 70
 SOFTWARE: patentin version 3.1
 SEQ ID NO 64
 LENGTH: 40
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-601-844B-64

RESULT 15 7.2%; Score 34; DB 4; Length 40;
 US-09-949-016-12733/c
 ; Sequence 12733, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: Venter, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 12733
 LENGTH: 17883
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-12733

Query	Match	Similarity	Score	DB	Length
Best Local Matches	54.0%	Conservative	32.8	4	17883
67	0	Pred.	No.	17	
Matches	0	Mismatches	57	Indels	0
Qy	33	CTTPTTATGTTGATGGAAAGGCCCTGTCAAGAGTGAGCCGGAAACTCAGGGTACA	92		
Db	109301	CTTGRCCGTGATGATGCTGGGTTGCAAATGTTGACTCACAGCCAGGGCTTACA		109242	
Qy	93	GTGCAACCTGCGAGCAGGCHACCGCTACCTTGACCCAGGGTCACTCTGGTGGATGA	152		
Db	109241	RACTGTCCTCCAGGAGAGAACATCATCCAGATCAGGGCACAGTTGGCGGTGTC		109182	
Qy	153	TGTT 156			
Db	109181	TGCT 109178			

Search completed: February 26, 2005, 05:20:30
Job time : 88.1144 secs

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 OM nucleic - nucleic search, using SW model
 GenCore version 5.1.6

Score, No. 18, the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
US-03-785-548-3
Sequence 3, Application US/09785548
; Patent No. US2002015557A1
; GENERAL INFORMATION:
; APPLICANT: AVENTIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: COMPOSITIONS THAT CAN BE USED FOR REGULATING THE ACTIVITY
FILE REFERENCE: ST0005
CURRENT APPLICATION NUMBER: US/09/785,548
CURRENT FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 471
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(471)

Db 121 ACCTTGAACTCCAGGGTCACTTCGTTGAGATGTTTATTCACACGGATGAGTGT 180
 Qy 181 GAATGCCAATCCCACACTGCCCCGGACTAGTGAGAATTTCCTTAATGGAGCA 180
 Db 181 GAATGCCAATCCCACACTGCCCCGGACTAGTGAGAATTTCCTTAATGGAGCA 240
 Qy 241 CACCCACCTCTGACAGGAAACATCGTAGCTGCACTTGATGCACAATAGTGG 240
 Db 241 CACCCACCTCTGACAGGAAACATCGTAGCTGCACTTGATGCACAATAGTGG 300
 Qy 301 AACATCAGTCACTTGCAGAGAACATGAGCTAGTTGACCTGACATGAC 300
 Db 301 AACATCAGTCACTTGCAGAGAACATGAGCTAGTTGACCTGACATGAC 360
 Qy 361 TCCGGCCCGTGAATTCGTTAGCTTCCACTTATAGTGTGACAGAACATGAT 360
 Db 361 TCCGGCCCGTGAATTCGTTAGCTTCCACTTATAGTGTGACAGAACATGAT 420
 Qy 421 CGCAGTTGTCAGGACTCAACTGGCTACTCCCTGCTGTTGAG 420
 Db 421 CGCAGTTGTCAGGACTCAACTGGCTACTCCCTGCTGTTGAG 471

RESULT 2
 US-10-622-817-10
 ; Sequence 10, Application US/10622817
 ; Publication No. US20040214763A1.
 ; GENERAL INFORMATION:
 ; APPLICANT: CORTI, Olga
 ; APPLICANT: HAMPE, Cornelia
 ; APPLICANT: BRICE, Alexis
 ; APPLICANT: PRADIER, Laurent
 ; APPLICANT: ROONEY, Thomas
 ; APPLICANT: FOURNIER, Alain
 ; TITLE OF INVENTION: METHOD FOR DETERMINING THE ABILITY OF A COMPOUND TO MODIFY THE CURRENT APPLICATION NUMBER: US/10622817
 ; CURRENT FILING DATE: 2003-07-18
 ; PRIORITY FILING DATE: 2002-12-20
 ; PRIORITY APPLICATION NUMBER: GB 0229934.5
 ; NUMBER OF SEQ ID NOS: 81
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 12
 ; LENGTH: 2955
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-839-688-12

Query Match 99.0%; Score 466; DB 19; Length 2955;
 Best Local Similarity 99.8%; Pred. No. 1.1e-154;
 Matches 467; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAAGTCAGCAGGATCATCATCACAGACGTTATGGATTGCAAGGCCCTGT 60
 Db 499 GGAACTCCAGAGGATGATCATCACAGACGTTATGGATTGCAAGGCCCTGT 558
 Qy 61 CAAGAGTCAGCCGGAAACTCAGGGTACACTGGATGTTATGTCATGCAAGGCCCTGT 558
 Db 559 CAAGAGTCAGCCGGAAACTCAGGGTACACTGGATGTTATGTCATGCAAGGCCCTGT 618
 Qy 121 ACCTTGACCGGGTCACTTCTGGATGATGTTTAATCCAAACCGGATGAGTGT 180
 Db 619 ACCTTGACCGGGTCACTTCTGGATGATGTTTAATCCAAACCGGATGAGTGT 180
 Qy 181 GAATGCCAATCCCACACTGCCCCGGACTAGTGAGAATTTCCTTAATGGAGCA 240
 Db 679 GAATGCCAATCCCACACTGCCCCGGACTAGTGAGAATTTCCTTAATGGAGCA 738
 Qy 241 CACCCACCTCTGACAGGAAACATCGTAGCTGCACTTGATGCACAATAGTGG 300
 Db 739 CACCCACCTCTGACAGGAAACATCGTAGCTGCACTTGATGCACAATAGTGG 300
 Qy 301 AACATCAGTCACTTGCAGAGAACATGAGCTAGTTGACCTGACATGAC 360
 Db 799 AACATCAGTCACTTGCAGAGAACATGAGCTAGTTGACCTGACATGAC 360
 Qy 361 TCCGGCCCGTGAATTCGTTAGCTTCCACTTATAGTGTGACAGAACATGAT 420
 Db 859 TCCGGCCCGTGAATTCGTTAGCTTCCACTTATAGTGTGACAGAACATGAT 420
 Qy 421 CGCAGTTGTCAGGACTCAACTGGCTACTCCCTGCTGTTGAG 468

Query Match 100.0%; Score 471; DB 18; length 471;
 Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAAGTCAGCAGGATCATCATCACAGACGTTATGGATTGCAAGGCCCTGT 60
 Db 61 CAAGAGTCAGCCGGAAACTCAGGGTACACTGGATGTTATGTCATGCAAGGCCCTGT 60
 Qy 121 ACCTTGACCGGGTCACTTCTGGATGATGTTTAATCCAAACCGGATGAGTGT 180
 Db 121 ACCTTGACCGGGTCACTTCTGGATGATGTTTAATCCAAACCGGATGAGTGT 180
 Qy 181 GAATGCCAATCCCACACTGCCCCGGACTAGTGAGAATTTCCTTAATGGAGCA 240
 Db 679 GAATGCCAATCCCACACTGCCCCGGACTAGTGAGAATTTCCTTAATGGAGCA 738
 Qy 241 CACCCACCTCTGACAGGAAACATCGTAGCTGCACTTGATGCACAATAGTGG 300
 Db 739 CACCCACCTCTGACAGGAAACATCGTAGCTGCACTTGATGCACAATAGTGG 300
 Qy 301 AACATCAGTCACTTGCAGAGAACATGAGCTAGTTGACCTGACATGAC 360
 Db 799 AACATCAGTCACTTGCAGAGAACATGAGCTAGTTGACCTGACATGAC 360
 Qy 361 TCCGGCCCGTGAATTCGTTAGCTTCCACTTATAGTGTGACAGAACATGAT 420
 Db 859 TCCGGCCCGTGAATTCGTTAGCTTCCACTTATAGTGTGACAGAACATGAT 420
 Qy 421 CGCAGTTGTCAGGACTCAACTGGCTACTCCCTGCTGTTGAG 918

Db 919 CGGCAGTTGTCACGACCCTAACTGGCTACTCCCTGCCCTGTG 96

RESULT 4

US-10-473-226-1

; Sequence 1; Application US/10473226

; Publication No. US20040198650A1

; GENERAL INFORMATION:

; TITLE OF INVENTION: Means for inhibiting proteolytical processing of Parkin

; FILE REFERENCE: 506-204-WO

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: DK PA 2001 00525

; PRIOR FILING DATE: 2001-03-29

; PRIOR APPLICATION NUMBER: US 60/281,286

; CURRENT APPLICATION NUMBER: US/10473,226

; CURRENT FILING DATE: 2003-09-29

; PRIOR APPLICATION NUMBER: DK PA 2001 00525

; PRIOR FILING DATE: 2001-03-29

; PRIOR APPLICATION NUMBER: US 60/281,286

; PRIOR FILING DATE: 2001-04-03

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 2960

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: mRNA

; LOCATION: (1)..(2960)

; OTHER INFORMATION:

US-10-473-226-1

Query Match 99.0%; Score 466.4; DB 18; Length 2960;

Best Local Similarity 99.8%; Pred. No. 1..1e-154; Mismatches 0; Indels 0; Gaps 0; Matches 467; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAAGTCCAGCAGGTAGATCACTACACGCTTATGTTGTTGCAAGGCCCCCT 60

Db 504 GGAGTCCGCAGCAGGTAGATCACTACACGCTTATGTTGTTGCAAGGCCCCCT 563

Qy 61 CAAGAGTGCAAGGGAAACTCAGGGTAACCTACACAGCTTTATGTTGTTGCAAGGCCCCCT 60

Db 504 GGAGTCCAGCAGGTAGATCACTACACGCTTATGTTGTTGCAAGGCCCCCT 563

Qy 61 CAAGAGTGCAAGGGAAACTCAGGGTAACCTACACAGCTTTATGTTGTTGCAAGGCCCCCT 120

Db 564 CAAGAGTGCAAGGGAAACTCAGGGTAACCTACACAGCTTATGTTGTTGCAAGGCCCCCT 623

Qy 121 ACCITGACCCAGGGTCATCTGCGGGATGTTATTCAAACCGGATGAGTGT 180

Db 624 ACCITGACCCAGGGTCATCTGCGGGATGTTATTCAAACCGGATGAGTGT 683

Qy 181 GAATGCCCATCCCCAACACTGCCCTGGACTAGTCAGAATTTCCTTAAATGGAGCA 240

Db 684 GAATGCCCATCCCCAACACTGCCCTGGACTAGTCAGAATTTCCTTAAATGGAGCA 743

Qy 241 CACCCCACTCTGCAAGAAACATCAGCTTGCCCTGGACTAGTCAGAATTTCCTTAAATGGAGCA 300

Db 744 CACCCCACTCTGCAAGAAACATCAGCTTGCCCTGGACTAGTCAGAATTTCCTTAAATGGAGCA 803

Qy 301 AACATCACTGCAATTGCAAGACGCTAGGGGCCGTCCTGGTTTCCAGTGAC 360

Db 804 AACATCACTGCAATTGCAAGACGCTAGGGGCCGTCCTGGTTTCCAGTGAC 863

Qy 361 TCCGCCCACTGTTAGCTAGTGTACCTATCTGTCAGACAGACTCAATGAT 420

Db 864 TCCGCCCACTGTTAGCTAGTGTACCTATCTGTCAGACAGACTCAATGAT 923

Qy 421 CGGAGTTGTCAGAACCTCACTTGCTACTTGCTACTTGCTGTTG 468

Db 924 CGGAGTTGTCAGAACCTCACTTGCTACTTGCTACTTGCTGTTG 971

RESULT 5

US-10-473-226-3

; Sequence 3; Application US/10473226

; Publication No. US20040198650A1

; GENERAL INFORMATION:

; TITLE OF INVENTION: INTERACTION BETWEEN PARKIN AND THE P38 PROTEIN

; FILE REFERENCE: FRAV2002-0020 US NP

; CURRENT APPLICATION NUMBER: US/10/622,817

; CURRENT FILING DATE: 2003-07-18

; PRIOR APPLICATION NUMBER: GB 0229934.5

; TITLE OF INVENTION: Means for inhibiting proteolytical processing of Parkin

RESULT 6

US-10-622-817-7

; Sequence 7; Application US/10622817

; Publication No. US20040214763A1

; GENERAL INFORMATION:

; APPLICANT: CORTI, Olga

; APPLICANT: HAMPE, Cornelia

; APPLICANT: BRICE, Alexis

; APPLICANT: PRADIER, Laurent

; APPLICANT: ROONEY, Thomas

; APPLICANT: FOURNIER, Alain

; TITLE OF INVENTION: METHOD FOR DETERMINING THE ABILITY OF A COMPOUND TO MODIFY THE

; TITLE OF INVENTION: INTERACTION BETWEEN PARKIN AND THE P38 PROTEIN

; FILE REFERENCE: FRAV2002-0020 US NP

; CURRENT APPLICATION NUMBER: US/10/622,817

; CURRENT FILING DATE: 2003-07-18

; PRIOR APPLICATION NUMBER: GB 0229934.5

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; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/396,929
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 7
; LENGTH: 2960
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (102)..(1499)
; US-10-622-817-7

Query Match 99 0%; Score 466.4; DB 18; Length 2960;
Best Local Similarity 99.8%; Pred. No. 1..le-154; Matches 467; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGAAGTCCGCACTGATCAACTACACAGCTTATGGTAGTCAGAACGCCCCTG 60
Db 504 GGAAGTCCGCACTGATCAACTACACAGCTTATGGTAGTCAGAACGCCCCTG 563
Qy 61 CAAGAGTCAGCGGGAAACTCAGGTAGTGCTGAGCTGCAGGAGGACGTC 120
Db 564 CAAGAGTCAGCGGGAAACTCAGGTAGTGCTGAGCTGCAGGAGGACGTC 623
Qy 121 ACCTTGACCCAGGGTCATCTTGCTGGAGATGTTATTCAAACAGATGAGGT 180
Db 624 ACCCTGACCCAGGGTCATCTTGCTGGAGATGTTATTCAAACAGATGAGGT 683
Qy 181 GATGCCAACTCCCACTCCTCGACTGAGCTAGTGCTGAGATTCTTAATGGAGCA 240
Db 684 GATGCCAACTCCCACTCCTCGACTGAGCTAGTGCTGAGATTCTTAATGGAGCA 743
Qy 241 GACCCCCACTCTGACAGGAACTCACTGAGCTTGCACTTGCACTGATCGAACATAGTCGG 300
Db 744 CACCCACCTCTGACAGGAACTCACTGAGCTTGCACTGATCGAACATAGTCGG 803
Qy 301 AACATCACTTGCAATTACGTCACAGACCTCAAGAGCCGCTGGTTTCAGTCAC 360
Db 804 AACATCACTTGCAATTACGTCACAGACCTCAAGAGCCGCTGGTTTCAGTCAC 863
Qy 361 TCCGCCACGTGATGCTGTTAATCTGCTTAACTGTGACAAGCATGAT 420
Db 864 TCCGCCACGTGATGCTGTTAATCTGCTTAACTGTGACAAGCATGAT 923
Qy 421 CGGAGTGTGTCAGGACCTCAACTTGCTTACTCTGCTGTTGAGCTCAATGAT 468
Db 924 CGGAGTGTGTCAGGACCTCAACTTGCTTACTCTGCTGTTGAGCTCAATGAT 971

RESULT 7
US-10-776-604-1
; Sequence 1, Application US/10776604
; Publication No. US20050003385A1
; GENERAL INFORMATION:
; APPLICANT: Shimizu, Nobuyoshi
; APPLICANT: Shimizu, Nobuyoshi
; TITLE OF INVENTION: DNAs or Genes Participating in Parkinson's Disease
; CURRENT APPLICATION NUMBER: US/10/776,604
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 09/601,844
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: PCT/JP99/00545
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: JP 10/27531
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 1
; LENGTH: 2960
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (102)..(1496)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (102)..(108)
; OTHER INFORMATION: Exon 1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (109)..(272)
; OTHER INFORMATION: Exon 2
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (273)..(513)
; OTHER INFORMATION: Exon 3
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (514)..(635)
; OTHER INFORMATION: Exon 4
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (636)..(719)
; OTHER INFORMATION: Exon 5
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (836)..(972)
; OTHER INFORMATION: (720)..(835)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (973)..(1034)
; OTHER INFORMATION: Exon 6
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1185)..(1268)
; OTHER INFORMATION: Exon 7
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1269)..(1366)
; OTHER INFORMATION: (1269)..(1366)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1387)..(2260)
; OTHER INFORMATION: Exon 12
; US-10-776-604-1

Query Match 99 0%; Score 466.4; DB 18; Length 2960;
Best Local Similarity 99.8%; Pred. No. 1..le-154; Matches 467; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGAAGTCCGCACTGATCAACTACACAGCTTATGGTAGTCAGAACGCCCCTG 60
Db 504 GGAAGTCCGCACTGATCAACTACACAGCTTATGGTAGTCAGAACGCCCCTG 563
Qy 61 CAAGAGTCAGCGGGAAACTCAGGTAGTGCTGAGCTGCAGGAGGACGTC 120
Db 564 CAAGAGTCAGCGGGAAACTCAGGTAGTGCTGAGCTGCAGGAGGACGTC 623
Qy 121 ACCTTGACCCAGGGTCATCTTGCTGGAGATGTTATTCAAACAGATGAGGT 180
Db 624 ACCCTGACCCAGGGTCATCTTGCTGGAGATGTTATTCAAACAGATGAGGT 683
Qy 181 GATGCCAACTCCCACTCCTCGACTGAGCTAGTGCTGAGATTCTTAATGGAGCA 240

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Db 684 GAACTCCAAATCCCCACACTGCCGAGCTAGTGCGAGAATTTCCTTAAATGTGAGCA 743
 Qy 241 CACCCACCTCTGCAAGAACACATCAGTAGCTTGACCTGTCAGTGCACAAATAGTCG 300
 Db 744 CACCCACCTCTGACAGAACACAGTAGCTTGACCTGTCAGTGCACAAATAGTCG 803
 Qy 301 AACATCACTTGCAATACGTGCCACAGACGTCAGGACCCCTCTGTTCCAGTGCAC 360
 Db 804 AACATCACTTGCAATACGTGCCACAGACGTCAGGACCCCTCTGTTCCAGTGCAC 863
 Qy 361 TCCGGCACCGTGTAGTTGCTGAGCTTGTTCCACTTAATCTGTGACAGACTCATGAT 420
 Db 864 TCCGGCACCGTGTAGTTGCTGAGCTTGTTCCACTTAATCTGTGACAGACTCATGAT 923
 Qy 421 CGGAGTTGTTGACGACCTCAACTTGACTCTGCTGCTGTTG 468
 Db 924 CGGAGTTGTTGACGACCTCAACTTGACTCTGCTGCTGTTG 971

RESULT 8
 US-10-839-688-11
 Sequence 11, Application US/10839688
 Publication No. US20050014173A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FARRER, Matthew J.
 ; TITLE OF INVENTION: PARKINSON'S DISEASE MARKERS
 ; FILE REFERENCE: 07019-445001
 ; CURRENT APPLICATION NUMBER: US10/839,688
 ; CURRENT FILING DATE: 2004-05-05
 ; PRIOR APPLICATION NUMBER: US 60/468,832
 ; PRIOR FILING DATE: 2003-05-08
 ; NUMBER OF SEQ ID NOS: 81
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 11
 ; LENGTH: 2960
 ; ORGANISM: Homo sapiens
 ; US-10-839-688-11

Query Match 99.0%; Score 466.4; DB 19; Length 2960;
 Best Local Similarity 99.8%; Pred. No. 1.1e-154; Mismatches 1; Indels 0; Gaps 0;
 Matches 467; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAAGTCCAGCAGGTAGATCACTACAACAGCTTTATGTGATTGCAAAGGCCCTGT 60
 Db 504 GGAAGTCCAGCAGGTAGATCACTACAACAGCTTTATGTGATTGCAAAGGCCCTGT 563

Qy 61 CAAGAGTGCAGCCGAAACTCGGGTACAGTGCAACGCTCAACGGCAACGCTC 120
 Db 564 CAAGAGTGCAGCCGAAACTCGGGTACAGTGCAACGCTCAACGGCAACGCTC 623

Qy 121 ACCTTGACCGGGTCATCTGCGGGATATCCAAACGGATGAGTGT 180
 Db 624 ACCTTGACCGGGTCATCTGCGGGATATCCAAACGGATGAGTGT 683

Qy 181 GAAATGCCAAATCCCACACTGCCCTGGACTAGTGCGAGAATTTCCTTAATGTGAGCA 240
 Db 684 GAAATGCCAAATCCCACACTGCCCTGGACTAGTGCGAGAATTTCCTTAATGTGAGCA 743

Qy 241 CACCCACCTCTGCAAGAACACATCAGTAGCTTGACCTGTCAGTGCACAAATAGTCG 300
 Db 744 CACCCACCTCTGACAGAACACAGTAGCTTGACCTGTCAGTGCACAAATAGTCG 803

Qy 301 AACATCACTTGCAATACGTGCCACAGACGTCAGGACCCCTCTGTTCCAGTGCAC 360
 Db 804 AACATCACTTGCAATACGTGCCACAGACGTCAGGACCCCTCTGTTCCAGTGCAC 863

Qy 361 TCCGGCACCGTGTAGTTGCTGAGCTTGTTCCACTTAATCTGTGACAGACTCATGAT 420
 Db 864 TCCGGCACCGTGTAGTTGCTGAGCTTGTTCCACTTAATCTGTGACAGACTCATGAT 923

Qy 421 CGGAGTTGTTGACGACCTCAACTTGACTCTGCTGCTGTTG 468
 Db 924 CGGAGTTGTTGACGACCTCAACTTGACTCTGCTGCTGTTG 971

RESULT 9
 US-10-622-817-13
 Sequence 13, Application US/10622817
 Publication No. US20040214763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CORTI, Olga
 ; APPLICANT: HAMPE, Cornelia
 ; APPLICANT: BRICE, Alexis
 ; APPLICANT: PRAIER, Laurent
 ; APPLICANT: ROONEY, Thomas
 ; APPLICANT: FOURNIER, Alain
 ; TITLE OF INVENTION: METHOD FOR DETERMINING THE ABILITY OF A COMPOUND TO MODIFY THE
 ; TITLE OF INVENTION: INTERACTION BETWEEN PARKIN AND THE P38 PROTEIN
 ; FILE REFERENCE: FRAY2002-0020 US NP
 ; CURRENT APPLICATION NUMBER: US/10/622,817
 ; CURRENT FILING DATE: 2003-07-18
 ; PRIOR APPLICATION NUMBER: GB 0229934.5
 ; PRIOR FILING DATE: 2002-12-20
 ; PRIOR APPLICATION NUMBER: US 60/396,929
 ; PRIOR FILING DATE: 2002-07-18
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 13
 ; LENGTH: 1470
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1470)
 ; US-10-622-817-13

Query Match 73.7%; Score 347; DB 18; Length 1470;
 Best Local Similarity 83.9%; Pred. No. 2.7e-112; Mismatches 75; Indels 0; Gaps 0;
 Matches 392; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Qy 2 GAAGTCCAGCAGGTAGATCACTACAACAGCTTTATGTGATTGCAAAGGCCCTGT 61
 Db 476 GAGGTCAGAAGCTAACCCACCTTACACAGCTTGTACTGCAAGGCCCTGT 535

Qy 62 AAAGAGTGCAGCCGAAACTCGGGTACAGTGCAACGCTCAACGGCAACGCTCA 121
 Db 536 ACAAGGTCTAGCTCGGTAACTCGACAGCTTGTACTGCAAGGCCCTGT 595

Qy 122 CCTTGACCCAGGTTCACTTGCTGGATGATGTTTATTCCAAACCGATGATGTTG 181
 Db 596 OCTTGGCCAGGGCCACCTTGCTGGATGATGCTTAACTCCAAACCGATGATGTTG 655

Qy 182 AATGCCAAATCCCACACTGCCCTGGACTAGTGCGAGAATTTCCTTAATGTGAGCA 241
 Db 656 AGTGTCAATCTCCAGACTCCCTGGACAGAGGTGATGTTTCTTAAATGTGAGCA 715

Qy 242 ACCCACTCTGCAAGAACATCAGTAGCTTGACCTGTCAGTGCACAAATAGTCG 301
 Db 716 ACCCAACTCTGCAAGAACACATCAGTAGCTTGACCTGTCAGTGCACAAATAGTCG 775

Qy 302 ACATCACTTGCAATTAGTGACAGACGTCAGGAGCCCTCTGTTCCAGTGCAC 361
 Db 776 GCATCCCCCTGCACTGGCTGACGGATGCAAGACCCCTCTGTTCCAGTGCAC 835

Qy 362 CCCCACTCTGCAAGAACACATCAGTAGCTTGACCTGTCAGTGCACAAATAGTCG 421
 Db 836 ACCGGCACGTTGACCTGTCAGTGCACAGCTGCTGCTGCTGCTGCTGCTGCTG 895

Qy 422 GGCGAGTTGTTGACGACCTCAACTTGACTCTGCTGCTGCTGCTGCTGCTGCTG 468
 Db 896 GGCGAGTTGTTGACGACCTCAACTTGACTCTGCTGCTGCTGCTGCTGCTGCTG 942

RESULT 10
 US-10-776-604-3

Sequence 3, Application US/10776604
 Publication No. US20050003385A1
 GENERAL INFORMATION:
 APPLICANT: Shimizu, Nobuyoshi
 APPLICANT: Mizuno, Yoshikuni
 TITLE OF INVENTION: DNAs or Genes Participating in Parkinson's Disease

FILE REFERENCE: 0652.21.0001
 CURRENT APPLICATION NUMBER: US/10/776,604
 CURRENT FILING DATE: 2004-02-12
 PRIOR APPLICATION NUMBER: 09/601,844
 PRIOR FILING DATE: 2000-08-09
 PRIOR APPLICATION NUMBER: PCT/JP99/00545
 PRIOR FILING DATE: 1999-02-09
 PRIOR APPLICATION NUMBER: JP 10/27531
 PRIOR FILING DATE: 1998-02-09
 NUMBER OF SEQ ID NOS: 70
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 3
 LENGTH: 2876
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (102)..(1412)
 OTHER INFORMATION:
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (102)..(108)
 OTHER INFORMATION: Exon 1
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (109)..(272)
 OTHER INFORMATION: Exon 2
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (273)..(513)
 OTHER INFORMATION: Exon 3
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (514)..(635)
 OTHER INFORMATION: Exon 4
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (636)..(751)
 OTHER INFORMATION: Exon 6
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (752)..(888)
 OTHER INFORMATION: Exon 7
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (889)..(950)
 OTHER INFORMATION: Exon 8
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (951)..(1100)
 OTHER INFORMATION: Exon 9
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1101)..(1184)
 OTHER INFORMATION: Exon 10
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1185)..(1302)
 OTHER INFORMATION: Exon 11
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1303)..(2876)
 OTHER INFORMATION: Exon 12

Query Match 61.2%; Score 288.4; DB 18; Length 2876;
 Best Local Similarity 81.8%; Prod. No. 2.9e-91; Length 2876;

RESULT 11
 US-10-839-688-6
 Sequence 6, Application US/10839688
 Publication No. US20050014173A1
 GENERAL INFORMATION:
 APPLICANT: Parter, Matthew J.
 TITLE OF INVENTION: PARKINSON'S DISEASE MARKERS

FILE REFERENCE: 07039-448001
 CURRENT APPLICATION NUMBER: US/10/839,688
 CURRENT FILING DATE: 2004-05-05
 PRIOR APPLICATION NUMBER: US 60/468,832
 PRIOR FILING DATE: 2003-05-08
 NUMBER OF SEQ ID NOS: 81
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 6
 LENGTH: 650
 TYPE: DNA
 ORGANISM: Homo sapiens

US-10-839-688-6

Query Match 29.4%; Score 138.6; DB 19; Length 650;
 Best Local Similarity 99.3%; Pred. No. 3.4e-38; Matches 138; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	Db
330 CAGGAGCCCGCTCGGTTCAGTGCAACTCCGCCCGTGAATTGGTTAGCTGT	61 CAAAGAGTGCAGCCGAAACTCAGGTACAGTGACCTGCAAGCAGCCCTGT
330 CAGGAGCCCGCTCGGTTCAGTGCAACTCCGCCCGTGAATTGGTTAGCTGT	504 GGAGGTCACAGGATGATCACTTACAGCTAACAGCTTATGTTAGTGAAAGCCCTGT
390 CCACATATCTGTGACAAGACTCAATATCGCAGTTGTACGACCTCACTTG	564 CAAGAGTGCAGCCGAAACTCAGGTACAGTGACCTGCAAGCAGCCCTGT
390 CCACATATCTGTGACAAGACTCAATATCGCAGTTGTACGACCTCACTTG	121 ACCTTGACCCAGGTCCATCTGTGGATGAGTTTAATCCAACCGGATGAGTGT
390 CCACATATCTGTGACAAGACTCAATATCGCAGTTGTACGACCTCACTTG	624 ACCTTGACCCAG-----
450 CTACTCCCTCTCTGTG	635 -----
450 CTACTCCCTCTCTGTG	180 624 ACCTTGACCCAG-----
328 CTACTCCCTCTCTGTG	636 -----
328 CTACTCCCTCTCTGTG	659 GAATTTCCTTAATGTGAGCA
421 CGCGAGTTGTCACGACGCTCACTTGCTACTCCCTGCCCTGTG	719 660 CACCCACCTCTGACAAGAACACAGCTTACAGCTGCAACATAATGCG
421 CGCGAGTTGTCACGACGCTCACTTGCTACTCCCTGCCCTGTG	779 720 AACATCACTTGCAATACCGACAGCTGCAAGCCGCTGTGTTCCAGTCAC
420 QY 361 TCCGGCCACGTGATTGTGACTGTTCACTTATCTGTGACAGACTCAATG	780 TCCGGCCACGTGATTGTGACTGTTCACTTATCTGTGACAGACTCAATG
468 Db 840 CGGCAAGTTGTCACGACCTCAACTTGCTACTCCCTGCCCTGTG	839 421 CGCGAGTTGTCACGACGCTCACTTGCTACTCCCTGCCCTGTG
887	468

US-10-839-688-4
; Sequence 4, Application US/10839688
; Publication No. US20050014173A1
; GENERAL INFORMATION:
; APPLICANT: Farber, Matthew J.
; FILE REFERENCE: 07039-448001
; CURRENT APPLICATION NUMBER: US/10/839, 688
; PRIOR APPLICATION NUMBER: US 60/468, 832
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-839-688-4

Query Match 19.1%; Score 89.8; DB 19; Length 660;
Best Local Similarity 91.3%; Pred. No. 8.4e-21; Mismatches 8; Indels 0; Gaps 0;
Matches 94; Conservative 1; MisMatches 8; Indels 0; Gaps 0;
Qy 124 TGACCCAGGGCTCATCTTGCTGGATGATGTTTAATTCCAAACCGGTAGGGTGA 183
Db 236 TTCCCAAGGGCTCATCTTGCTGGATGATGTTTAATTCCAAACCGGTAGGGTGA 295
Qy 184 TGCCTATCCCACACTGCCCTGGACTACTGAGAATTCT 226
Db 296 TGCCATTCACACTGCCCTGGACTACTGAGAATTCT 338

RESULT 13

US-09-908-975-26043

; Sequence 26043, Application US/09908975

; Publication No. US20030165843A1

; GENERAL INFORMATION:

; APPLICANT: SHOSHAN, Avi

; APPLICANT: WASSERMAN, Alon

; APPLICANT: MINNIZ, Eli

; APPLICANT: MINNIZ, Liat

; APPLICANT: FAIGLER, Simchon

; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC

; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME

; FILE REFERENCE: 36688-0005

; CURRENT APPLICATION NUMBER: US/09/908, 975

; CURRENT FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 60/287, 724

; PRIOR FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: US 60/221, 607

; NUMBER OF SEQ ID NOS: 32337

; SOFTWARE: PatentIn Version 3.0

; SEQ ID NO 26043

; LENGTH: 65

; TYPE: DNA

; ORGANISM: Mus musculus

; US-09-908-975-26043

RESULT 14

US-10-776-604-65

; Sequence 65, Application US/10776604

; Publication No. US20050003385A1

; GENERAL INFORMATION:

; APPLICANT: Shimizu, Nobuyoshi

; FILE REFERENCE: 0652.2110001

; CURRENT APPLICATION NUMBER: US/10/776, 604

; CURRENT FILING DATE: 2004-02-12

; PRIOR APPLICATION NUMBER: 09/601, 844

; PRIOR FILING DATE: 2000-08-09

; PRIOR APPLICATION NUMBER: PCT/JP99/00545

; PRIOR FILING DATE: 1999-02-09

; PRIOR APPLICATION NUMBER: JP 10/27531

; PRIOR FILING DATE: 1998-02-09

; NUMBER OF SEQ ID NOS: 70

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 65

; LENGTH: 40

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-10-776-604-65

; Query Match 7.4%; Score 34.8; DB 18; Length 40;

; Best Local Similarity 94.7%; Pred. No. 0.001; Mismatches 0; Indels 0; Gaps 0;

; Matches 36; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

; Qy 128 CCCAGGGTCATCTGCTGGATGATGTTTAATTCCA 165

; Db 3 CCAAGGGTCATCTGCTGGATGATGTTTAATTCCA 40

; RESULT 15

US-09-735-705-293

; Sequence 293, Application US/09735705

; Patent No. US20020053329A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hooken, Nancy

; APPLICANT: Fangier, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Ajun

; APPLICANT: Skeky, Yasir A.W.

; APPLICANT: Henderson, Robert A.

; APPLICANT: Mcneill, Patricia D.

; APPLICANT: Fangier, Neil

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C14

; CURRENT APPLICATION NUMBER: US/09/735, 705

; CURRENT FILING DATE: 2000-12-12

; NUMBER OF SEQ ID NOS: 419

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 293

; LENGTH: 361

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)..(361)

; OTHER INFORMATION: n = A,T,C or G

; US-09-735-705-293

; Query Match 7.4%; Score 34.8; DB 9; Length 361;

; Best Local Similarity 59.4%; Pred. No. 0.25; Mismatches 39; Indels 0; Gaps 0;

; Matches 57; Conservative 0; MisMatches 39; Indels 0; Gaps 0;

; Qy 203 CTGGACTAGTCGNGAATTTCTTTAATGTCGAGCACCCACCTCTGACAGGAA 262

; Db 61 CCA 63

; RESULT 14

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Db	134	CTGACACCCCTCAATTCCCTCCAAATGCTGCATGCCACACTGAGGTAAACGAAG	193
QY	263	CATCAGTAGCTTGCACCTGATCGAACAAATAGTC	298
Db	194	CANAGTATTAAACATGACAGCTAANACATTC	229

Search completed: February 26, 2005, 13:19:16
Job time : 286.738 secs